

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2005, 05:59:29 ; Search time 232 Seconds

(without alignments)
319.312 Million cell updates/sec

Title: US-09-196-161d-1

Perfect score: 558
Sequence: 1 GAAQGEANGNPFPANNANAR.....PGGEAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	395	2	Q27208 ICHMU
2	558	100.0	442	2	Q9XG22 ICHMU
3	222	39.8	460	2	Q962N5 ICHMU
4	221	39.6	468	2	Q9BMH3 ICHMU
5	95	17.0	614	2	Q4VM07 VIPLE
6	93.5	16.8	371	2	Q9GPP0 TETTH
7	93	16.7	548	2	Q9G045 GIALA
8	93	16.7	677	2	Q7M3R4 GIALA
9	88.5	15.9	305	2	Q9GPP2 TETTH
10	88.5	15.9	316	2	Q9GPP3 TETTH
11	87	15.6	724	2	Q7QTV1 GIALA
12	85.5	15.3	518	2	Q8GIR8 SYN7
13	85.5	15.3	518	2	Q5N1J8 SYN6
14	85	15.2	316	2	Q9GPP4 TETTH
15	85	15.2	536	2	Q7QSV6 GIALA
16	85	15.2	692	2	Q7Q073 GIALA
17	85	15.2	692	2	Q818W4 GIALA
18	84.5	15.1	245	2	Q7Q0C5 GIALA
19	84.5	15.1	2330	1	EGFL4 MOUSE
20	84.5	15.1	2386	1	EGFL4 HUMAN
21	83	14.9	1190	1	LAMC2 HORSE
22	81.5	14.6	814	2	Q7R1V1 GIALA
23	81	14.5	130	2	Q9BIK1 GIALA
24	81	14.5	1429	2	Q4UHQ0 THEAN
25	81	14.5	1827	2	Q8JHV6 BRAR
26	80.5	14.4	560	2	Q9U0J3 GIALA
27	80.5	14.4	2855	2	Q61D08 CAEBR
28	80	14.3	338	2	Q6EQJ7 ORYSA
29	80	14.3	1118	2	Q61B94 CAEBR
30	79.5	14.2	759	2	Q4SBL9 TETNG
31	79.5	14.2	874	1	EGFL4 RAT

32	79.5	14.2	1019	2	Q9NA40 CAEBL	Q9NA40 caenorhabdi
33	79	14.2	155	2	Q88B0 PSESM	Q88B0 pseudomonas
34	79	14.2	600	2	Q9PVK7 NAJNA	Q9PVK7 naja naja (
35	79	14.2	3333	1	LAMM3 MOUSE	Q61789 mus musculu
36	78.5	14.1	239	2	Q7R376 GIALA	Q7R376 giardia lam
37	78.5	14.1	821	2	Q8VPM9 JMTC	Q8VPM9 micrococcus
38	78.5	14.1	1336	2	Q61UE2 CAEBR	Q61UE2 caenorhabdi
39	78	14.0	596	2	Q07317 GIALA	Q07317 giardia lam
40	78	14.0	833	2	Q6J288 ACACA	Q6J288 acanthamoeb
41	78	14.0	3718	1	LAMM5 MOUSE	Q61001 mus musculu
42	77.5	13.9	484	2	Q9SLG2 SHEEP	Q9SLG2 ovie aries
43	77.5	13.9	569	2	Q7QXT3 GIALA	Q7QXT3 giardia lam
44	77.5	13.9	573	2	Q9HWQ0 PSEAE	Q9HWQ0 pseudomonas
45	77.5	13.9	1997	2	Q81RM7 CHIRE	Q81RM7 chlamydomon

ALIGNMENTS

RESULT 1									
ID	Q27208	ICHMU	PRELIMINARY;	PRT;	395	AA.			
AC	Q27208;								
DT	01-NOV-1996	(Tremblrel. 01,	Created)						
DT	01-DEC-2001	(Tremblrel. 19,	Last sequence update)						
DT	01-MAR-2004	(Tremblrel. 26,	Last annotation update)						
DE	Immobilization antigen precursor (Fragment).								
OS	Ichthyophthirius multifiliis (White spot) (Ich).								
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;								
OC	Ophryoglenina; Ichthyophthirius.								
OX	NCBI_TaxID=5932;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=Georgia;								
RX	MEDLINE=92335298; PubMed=1631132;								
RA	Clark T.G., McGraw R.A., Dickerson H.W.;								
RT	"Developmental expression of surface antigen genes in the parasitic ciliate Ichthyophthirius multifiliis."								
RL	Proc. Natl. Acad. Sci. U.S.A. 89:6363-6367(1992).								
RN	[2]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=Georgia;								
RX	MEDLINE=93020590; PubMed=1383510;								
RA	Lin T.L., Dickerson H.W.;								
RT	"Purification and partial characterization of immobilization antigens from Ichthyophthirius multifiliis."								
RL	J. Protozool. 39:457-463(1992).								
RN	[3]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=Georgia;								
RA	Clark T.;								
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; M92907; AAC36158.1; -; mRNA.								
DR	PIR; A46031; A46031.								
DR	GO; GO:0005489; F:electron transporter activity; IEA.								
DR	GO; GO:0005506; F:iron ion binding; IEA.								
DR	GO; GO:0006118; P:electron transport; IEA.								
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.								
KW	PRINTS; PR00353; 4FE4SFRDOXIN.								
KW	Signal.								
FT	SIGNAL.	<1	1	Potential.					
FT	CHAIN	2	395	Immobilization antigen.					
FT	NON TER	1	1						
SQ	SEQUENCE	395	AA;	39567	MM;	68DA2C790E4FD393	CRC64;		
Query Match 100.0%; Score 558; DB 2; Length 395;									
Best Local Similarity 100.0%; Pred. No. 1.5e-48;									
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAAQGEANGNPFPANNANARGICVPCQINRVGSVTNAGDIATATGCGSTGCPGTALDDG	60						
DB	37	GAAQGEANGNPFPANNANARGICVPCQINRVGSVTNAGDIATATGCGSTGCPGTALDDG	96						

ID 04VM07_VIPLE PRELIMINARY; PRT; 614 AA.
AC 04VM07;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VLAIP-B.
OS Vipera lebetina (Elephant snake) (Leventine viper).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Eucleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Macrovipera.
OX NCBI_TaxID=8709;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15922394; DOI=10.1016/j.toxicol.2005.03.008;
RA Truimal K., Tomlasmagi K., Siliur E., Aaspollu A., Lopp A., Sillat T.,
RA Saat R., Kaasak L., Tammieste I., Kogerman P., Kalkkinnen N., Siliur J.,
RT "A novel metalloprotease from Vipera lebetina venom induces human
endothelial cell apoptosis."
RL Toxicol 46:46-61(2005).
CC -1- SIMILARITY: Contains 1 peptidase M12B domain.
DR EMBL; AF835977; AA38182.1; -, mRNA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006025; Pept_M Zn_BS.
DR InterPro; IPR002870; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin_1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 614 AA; 68843 MW; CE4F912493CDAC9 CRC64;

Query Match 17.0%; Score 95; DB 2; Length 614;
Best Local Similarity 30.6%; Pred. No. 0.45;
Matches 26; Conservative 9; Mismatches 36; Indels 14; Gaps 3;

QY 23 CVPQINRVSVTNAG----DLATLTCSTGCTGTALDDGTVDFDRSAACVCKKPN 78
DB 452 CYCKFRAGTGVKRPANGCEDVSLCTGOSABCP-----TDQFRNGQPCONNK-G 501
QY 79 FYYNGSGPQGEAPGVVFAGAGAAA 103
DB 502 YCYNGTCPIWEKOCISLFGASATYA 526

RESULT 6
09GPP0_TETTH PRELIMINARY; PRT; 371 AA.
AC 09GPP0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immobilization antigen LD.
GN Nemes-Serid;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenida; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=ANP18211;
RX MEDLINE=20549003; PubMed=11095959; DOI=10.1006/dbrc.2000.3857;
RA Doerder F.P., Gerber C.A.;
RT "Molecular characterization of the SerL paralogs of Tetrahymena
thermophila."
BL Biochem. Biophys. Res. Commun. 278:621-626(2000).

DR EMBL; AF312775; AAG38107.1; -, mRNA.
SQ SEQUENCE 371 AA; 35175 MW; 5817EFC2517DEAC CRC64;

Query Match 16.8%; Score 93.5; DB 2; Length 371;
Best Local Similarity 30.4%; Pred. No. 0.38;
Matches 41; Conservative 5; Mismatches 48; Indels 41; Gaps 6;

QY 1 GAAQGEANGQPFANNAARGICVPCQINRVSVTNAG-----DLA 41
DB 50 GACQCKPTGNSVAA-TASGTLVTSCTCDN---TNAGLKADNSGCCQKAPFGTPRAVA 104
QY 42 TLATGCTGCTGTALDDGTVDF-----DRSAQCVCKKPNFYNGSGPQG 88
DB 105 GAGTGC-TACPTGTATPAGAAVTSACANDTNASLKGDSGCC---CKANFYGTAPAAVAG 160
QY 89 EAPGVVFAGAGAAA 103
DB 161 GATGCTACPTGSAAA 175

RESULT 7
09GQ45_GIALA PRELIMINARY; PRT; 548 AA.
AC 09GQ45;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant-specific surface protein W21-1 (Fragment).
GN Name=M21-1;
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mansouri M., Ey P.L.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAG37862.1; -, Genomic_DNA.
DR HSP; O16119; IEZG.
DR InterPro; IPR006056; 2Fe2S_fd_BS.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 16.7%; Score 93; DB 2; Length 548;
Best Local Similarity 28.6%; Pred. No. 0.64;
Matches 30; Conservative 6; Mismatches 37; Indels 32; Gaps 6;

QY 5 GEANGQPFANNAARGICVPCQINRVSVTNAGDLA-----TLATOC----- 47
DB 273 GCTNGNHFVEGNNQK-LVPC-----GDTTNGVAGCMTCSKTTCTKCLDGYDSGSG 326
QY 48 ---STGCTGTALDDGTVDFDRSAACVCKKPNFYNGSGPQGE 89
DB 327 TVTCTACPGANC-----ATLCERYKQCTCKRGFFLKSS-SGE 365

RESULT 8
07M3R4_GIALA PRELIMINARY; PRT; 677 AA.
AC 07M3R4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Trophozoite cysteine-rich surface antigen 72 (Fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.

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OX NCBI_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92186850; PubMed=1545800;
RA Adam R.D., Yang Y.M., Nash T.E.;
RT "The cysteine-rich protein gene family of Giardia lamblia: loss of the
RL CRP170 gene in an antigenic variant.";
RL Mol. Cell. Biol. 12:1194-1201(1992).
DR PIR: C42125; C42125.
DR InterPro: IPR006058; 2Fe2S fd BS.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03302; VSP; 2.
DR PROSITE: PS00197; 2Fe2S_FERREDOXIN; UNKNOWN_1.
FT NON_TER 1 677
FT SEQUENCE 677 AA; 68410 MW; E6E621818C0271F5 CRC64;

Query Match
Best Local Similarity 16.7%; Score 93; DB 2; Length 677;
Matches 25; Conservative 9; Mismatches 36; Indels 18; Gaps 4;

QY 6 EANGNQP---FAANNAARGICVPCQINRVGSVTNAGDLATLTATQ-CSTQCPTGTALDDGV 61
DB 304 EANKGTGCKTKCKKQKAKPTCSBC---LDGYNSGNGGTVCACGANCATCTQAGND- 358
QY 62 TDVFDRSAQCVCKKPNFYNGSGPQGE 89
DB 359 -----KCTKCKRPGFPMKNGPTGE 377

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RESULT 9

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O9GPP2_TETTH
ID O9GPP2_TETTH PRELIMINARY; PRT; 305 AA.
AC O9GPP2_
RT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Immobilization antigen LC (Fragment).
GN Name=SerLC;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B;
RX MEDLINE=20549003; PubMed=11095959; DOI=10.1006/birc.2000.3857;
RA Doerder F.P., Geisler C.A.;
RT "Molecular characterization of the SerL paralogs of Tetrahymena
RL thermophila.";
RT Biochem. Biophys. Res. Commun. 278:621-626(2000).
DR EMBL: AF312772; AAC38118.1; -; mRNA.
FT NON_TER 305
FT SEQUENCE 305 AA; 28863 MW; 0566C33A0253564 CRC64;

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Query Match
Best Local Similarity 15.9%; Score 88.5; DB 2; Length 305;
Matches 38; Conservative 10; Mismatches 36; Indels 23; Gaps 8;

QY 10 NOPFAANNAARGICVPCQINRVGSVTNAGDLATLTATQCTCPTGTALDDGVTVF---- 65
DB 190 NSSLKADNSA---CV-CRANFYGT-PNA--VAGGATGC-TACPTGTTSTAGTTVIGSCAC 241
QY 66 -DRSAA-----QCVCKKPNFY-----YNGSGPQGEAPGVQVFAAGAA 101
DB 242 PDTNALNSATPVPVCQKANFYGTPTASGASGCTACPSGQTAPAGSA 288

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RESULT 10
O9GPP3_TETTH
ID O9GPP3_TETTH PRELIMINARY; PRT; 316 AA.
AC O9GPP3_
DT 01-MAR-2001 (Tremblrel. 16, Created)

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DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Immobilization antigen LB.
GN Name=SerLB;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B;
RX MEDLINE=20549003; PubMed=11095959; DOI=10.1006/birc.2000.3857;
RA Doerder F.P., Geisler C.A.;
RT "Molecular characterization of the SerL paralogs of Tetrahymena
RL thermophila.";
RL Biochem. Biophys. Res. Commun. 278:621-626(2000).
DR EMBL: AF312772; AAC38117.1; -; mRNA.
FT SEQUENCE 316 AA; 30008 MW; 133A0B7D0797A3BD CRC64;

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```

Query Match
Best Local Similarity 15.9%; Score 88.5; DB 2; Length 316;
Matches 38; Conservative 10; Mismatches 36; Indels 23; Gaps 8;

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QY 10 NOPFAANNAARGICVPCQINRVGSVTNAGDLATLTATQCTCPTGTALDDGVTVF---- 65
DB 190 NSSLKADNSA---CV-CRANFYGT-PNA--VAGGATGC-TACPTGTTSTAGTTVIGSCAC 241
QY 66 -DRSAA-----QCVCKKPNFY-----YNGSGPQGEAPGVQVFAAGAA 101
DB 242 PDTNALNSATPVPVCQKANFYGTPTASGASGCTACPSGQTAPAGSA 288

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RESULT 11

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O7OTU1_GIALA
ID O7OTU1_GIALA PRELIMINARY; PRT; 724 AA.
AC O7OTU1_
RT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE GLP 191.3328.5502.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB01000101; EAA38433.1; -; Genomic_DNA.
DR HSP: O14763; 1D0G.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03302; VSP; 1.
FT SEQUENCE 724 AA; 74382 MW; F689C8BFCA051E3 CRC64;

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Query Match
Best Local Similarity 15.6%; Score 87; DB 2; Length 724;
Matches 31; Conservative 13; Mismatches 39; Indels 38; Gaps 6;

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QY 3 AAGE-ANGNQPFAANNAARGICVPCQINRVGSVT-----NAGDLAT 42
DB 297 AEGECASGNTHTLEQSPK--ACVPCGADANGGILCSTCSKTTCTCKCIDGYNSGNGGT 354
QY 43 L-ATQCTQCPTGTALDDGVTVFDRSAAQCVCKKPNFYNGSGPQGEAPGVQVFAAGAA 101
DB 355 VTCTACGANCATCSAAGND-----QCTKCKRPGFPMKQPGSAGKC-----FACDSK 399
QY 102 A 102

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Db          400 A 400

RESULT 12
08GIR8 SYNPF7
ID 08GIR8 SYNPF7 PRELIMINARY; PRT; 518 AA.
AC 08GIR8
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fe5y.
GN Name=fe5y;
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
CC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83082639; PubMed=6129240;
RA Hall G.C., Flick M.B., Jensen R.A.;
RT "Regulation of the aromatic pathway in the cyanobacterium
RL Synechococcus sp. strain Pcc6301 (Anacystis nidulans).";
RN R1. Bacteriol. 153:423-428(1983).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RA Holtman C.K., Socias T., Mohler B.J., Chen Y., Min H., Golden S.S.,
RA Yoderlian P., Sandoval P., Gonzalez A., Salinas I.;
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; U30252; AAN71792.1; -; Genomic_DNA.
DR HSSP; P83749; 10KK.
DR GO; GO:0005766; C:signal recognition particle (sensu Eukaryota); IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. .; IEA.
DR InterPro; IPR003593; AA_Artpase.
DR InterPro; IPR004390; ABC_transport_Fc5y.
DR InterPro; IPR000897; SRP54.
DR Pfam; PF00448; SRP54; 1.
DR Pfam; PF02881; SRP54.N; 1.
DR Prodom; PD000819; SRP54; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR0064; Fe5y; 1.
DR PROSITE; PS00300; SRP54; 1.
SQ SEQUENCE 518 AA; 55589 MW; 8472A42C0B3D50D3 CRC64;

Query Match 15.3%; Score 85.5; DB 2; Length 518;
Best Local Similarity 30.4%; Pied. No.3.5;
Matche 31; Conservative 10; Mismatches 48; Indels 13; Gaps 3

Oy 6 EANGQPPAANNAAGCIVCPQINVGSVYTNAGDLATATGCTGCTGATLDDGVTF 65
Db 301 ETSGGYILAPBEGRLNWLVCVNGVGKTTTGKLAHLATKSGYKCLTAA-----DTF 354
Oy 66 DRSAAQCVK-----CKPNFYNGSGPQGEAPGVQVFAAGAA 102
Db 355 RAAAVEQYKVMGDRSEVDIVANPG--QNTDPAAVVFDAIAA 394

RESULT 13
05NIJ8 SYNPF6
ID 05NIJ8 SYNPF6 PRELIMINARY; PRT; 518 AA.
AC 05NIJ8
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Signal recognition particle subunit SRP54.
GN Name=fe5y; OrderedLocusNames=sgc1632.C;
OS Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
CC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=263084;
RN (1)
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=PC66301;
RA *Stigita* M.;
RT "Complete genome structure of the unicellular cyanobacterium *Anacyctis*
RT *nubilans* 6301 (Synchococcus sp. PC66301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000871; BAB79822.1; -; Genomic DNA.
DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000165; F:nucleotide binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006514; P:SRP-dependent cotranslational protein-membr. . .; IEA
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR004390; ABC_Transp_Ftey.
DR InterPro; IPR00897; SRP54.
DR Pfam; PF00448; SRP54; 1.
DR Pfam; PF02881; SRP54 N; 1.
DR Prodom; PD000819; SRP54; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00064; ftey; 1.
DR PROSITE; PS00300; SRP54; 1.
KW Complete proteome.
SQ SEQUENCE 518 AA; 55572 MW; 2503D56A7DAC39 CRC64;

Query Match	15.3%	Score 85.5	DB 2	Length 518
Best Local Similarity	30.4%	Pred. No. 3.5		
Matches	31	Conservative	10	Mismatches 48; Indels 13; Gaps 3
Db	6	EANGNQPAANNAARGICVPCQINVEGVTNAGDLATLATQCS	TOCPTGALDDGVTDF	65
Qy	66	DRSAAQCVK----	CKPNEYNGSGEAGEVQVFAAGAA	102
Db	355	RAAAVEQVKWMDRESEVDVIANPG--	QNTDPAVVFDAIAAA	394
RESULT 14				
ID	Q9GPP4	TETTH	PREDIMINARY;	PRT; 316 AA.
AC	Q9GPP4			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Immobiliation antigen LA.			
GN	Name=SerLA;			
OS	Tetrahymena thermophila.			
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;			
OC	Tetrahymenina; Tetrahymenidae; Tetrahymena.			
OX	NCBI_TaxID=5911;			
RN	(1)			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=B;			
RX	MEDLINE=20549003; PubMed=11095959; DOI=10.1006/dbrc.2000.3857;			
RA	Doeder F.F., Getzer C.A.;			
RT	"Molecular characterization of the SerL paralogs of Tetrahymena thermophila."			
RL	Biochem. Biophys. Res. Commun. 278:621-626(2000).			
DR	EMBL; AF312770; AAC38116.1; -; mRNA.			
SQ	SEQUENCE 316 AA; 30100 MW; 1A13D076F28EDBD CRC64;			
Query Match	15.2%	Score 85	DB 2	Length 316
Best Local Similarity	25.5%	Pred. No. 2.4		
Matches	38	Conservative	10	Mismatches 41; Indels 60; Gaps 7
Qy	4	OGEANGNDP----	FAANNAARGICVPCQINRGVSTNAGDLATLATQCS	48
Db	84	KGDNSGCCCKANFYGTPTNAVSGATGCTGCTTSPAGTAATVSCACNDTNASLKGDN	143	
Qy	49	-----	TOCPTGALDDGVTDV	-----
Db	144	GGOCCANFYGTPTNAVSGATGCTGCTTSPAGTAATVSCACNDTNSSLKADNSA--	CV 201	

QY 74 KCKPNFYNGSPQGEAPGVVFAAGAAA 102
 DB 202 -CKANFY---GTNNVAVAG---ATGCTA 222

RESULT 15

ID 07Q5X6_GIALA PRELIMINARY; PRT; 536 AA.
 AC 07Q5X6;
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE GUP_4_3458_1848.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AACB0100013; EAA3812.1; -; Genomic_DNA.
 DR InterPro: IPR011641; GCC2_GCC3.
 DR Pfam: PR07699; GCC2_GCC3_1.
 SQ SEQUENCE 536 AA; 58170 MW; F72DB5558B3E0C65 CRC64;

Query Match 15.2%; Score 85; DB 2; Length 536;
 Best Local Similarity 31.3%; Pred. No. 4.1;
 Matches 26; Conservative 8; Mismatches 37; Indels 12; Gaps 4;

QY 23 CVPCCQINRVGSVTNAGDLATLTCSTQCPTGTALDDGVTVDFDRSAQCCKKPNFYNN 82
 DB 419 CVPCCPNK---TTVHDGARLECYC--ECAPGFVLRDA-----DNIDAGCICQCORNSYSK 467
 QY 83 GG-SPOGEAPGVVFAAGAAAAG 104
 DB 468 GGTTTCQCCPSGNRPPTGKSGVG 490

Search completed: December 5, 2005, 06:16:19
 Job time : 235 secs


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Qy      11 QPFAANNAARGICVPCQINRVGSVTNAG---DLATLATQSGTCCPTGTALDDGVTVDFD 66
Db      443 QPHAGCD-SEGCCCKCKFKGAGAEACRAAKDDCDLDELCTGQSAECF-----TDIFQ 492
Qy      67 RSAACVCKCKPNFYNNGSP-----QGAEAGVQV 95
Db      493 RNLGLPC-QNNEGVCYNKCPIMTNCIALRGVAV 527

RESULT 5
US-09-026-001A-18
: Sequence 18, Application US/09026001A
: Patent No. 6413760
: GENERAL INFORMATION:
: APPLICANT: Boodhoo, Amechand
: APPLICANT: Seehra, Jaabir
: APPLICANT: Saw, Gray
: APPLICANT: Saku, Dianne
: TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
: TITLE OF INVENTION: THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026, 001A
: FILING DATE: 18-FEB-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G15293B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 621 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-026-001A-18

Query Match      15.1%; Score 84; DB 2; Length 621;
Best Local Similarity 29.2%; Pred. No. 0.91;
Matches 28; Conservative 10; Mismatches 36; Indels 22; Gaps 5

Qy      11 QPFAANNAARGICVPCQINRVGSVTNAG---DLATLATQSGTCCPTGTALDDGVTVDFD 66
Db      451 QPHAGCD-SEGCCCKCKFKGAGAEACRAAKDDCDLDELCTGQSAECF-----TDIFQ 500
Qy      67 RSAACVCKCKPNFYNNGSP-----QGAEAGVQV 95
Db      501 RNLGLPC-QNNEGVCYNKCPIMTNCIALRGVAV 535

RESULT 6
US-09-996-620-18
: Sequence 18, Application US/09996620

```

```

: Patent No. 6881404
: GENERAL INFORMATION:
: APPLICANT: Boonhoo, Amechand
:          Shau, Gray
:          Sako, Dianne
: TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
:                   PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED PROTEA
:                   THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/996,620
: FILING DATE: 27-No. 6881404-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/026,001
: FILING DATE: 18-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G15293B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 621 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-996-620-18
:
: Query Match          15.1%; Score 84; DB 2; Length 621;
: Best Local Similarity 29.2%; Pred. No. 0.91;
: Matches 28; Conservative 10; Mismatches 36; Indels 22; Gaps 5;
:
QY      11 QPFAANNAARGICVPCQINRVGSVTNAG---DIATLATGCGTCGPTGALTDDGVTVDV 66
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      451 QPHAGCD-SEGCCKCKFKGAGACRAKDDCDLPELCTGSAECF-----TDIFQ 500
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      67 RSAAGCVKCKRPFYNGSP-----QGEAPGYOV 95
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      501 RNLGPC-QNNEGVCYNGKCPITNOCIALRGPGKV 535
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 7
US-10-053-662A-2
: Sequence 2, Application US/10053662A
: Patent No. 691618
: GENERAL INFORMATION:
: APPLICANT: Alexandra Charlesworth
: APPLICANT: Faivia Spirito
: APPLICANT: Guerino Meneguzzi
: APPLICANT: John Baird
: APPLICANT: Keith Linder
: TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
: TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
: TITLE OF INVENTION: BULLOSA
: FILE REFERENCE: p84us4

```

/ CURRENT APPLICATION NUMBER: US/10/053,662A
/ CURRENT FILING DATE: 2002-01-24
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1190
/ TYPE: PRP
/ ORGANISM: Equine
/ FEATURE:
/ OTHER INFORMATION:
US-10-053-662A-2

Query Match 14.9%; Score 83; DB 2; Length 1190;
Best Local Similarity 24.4%; Pred. No. 2.5;
Matches 31; Conservative 16; Mismatches 28; Indels 52; Gaps 7;

QY 20 RQICVPCQINRVGS-----VTNAG--DLATLAT 45
DB 78 RDRCLPCNCSXGSLARCDNSGRCSCKPVTGDRCLPGPHLTLDAGCAQDRLDLS 137
QY 46 QC-----STOCPTGTL-DGVTDFPDRSAACVCKCKPNFY-NGSGPGEAPGVYF 96
DB 138 KCDDBAGISGPCDSGRVCCKPAVT-----GERCDRCRPGYHLDGNPQG---CTQCF 188
QY 97 AAGAAA 103
DB 189 CYGHSAS 195

RESULT 8
US-09-976-594-616
/ Sequence 616, Application US/09976594
/ Patent No. 6673549

/ GENERAL INFORMATION:
/ APPLICANT: Furness, Michael
/ APPLICANT: Buchdinder, Jenny
/ TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
/ FILE REFERENCE: PA-0041 US
/ CURRENT APPLICATION NUMBER: US/09/976,594
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240,409
/ PRIOR FILING DATE: 2000-10-12
/ NUMBER OF SEQ ID NOS: 1143
/ SOFTWARE: PERL Program
/ SEQ ID NO 616
/ LENGTH: 605
/ TYPE: PRP
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6673549 1692213CH1
/ NAME/KEY: unsure
/ LOCATION: 596
/ OTHER INFORMATION: unknown or other
US-09-976-594-616

Query Match 14.1%; Score 78.5; DB 2; Length 605;
Best Local Similarity 27.9%; Pred. No. 3.4;
Matches 36; Conservative 3; Mismatches 65; Indels 25; Gaps 3;

QY 1 GAAOGEANGNPFPANNAARGICVPCQINRVGSVTNAGDLA---TLATQC-----STOC 51
DB 409 GGTGGAAGGAAGAAATAAATCATATGAAGAAGCTGAATTAAGTTTATACATTTTGTTC 468
QY 52 PGTALDDVTDFDSAAOCVCKCKPNFYNGSGPGEAPG-----VOY 95
DB 469 TTTAAAGGATATACATATCTTTTGTAGCTGAGCTGCAAGAAATACAAAATTTTAA 528
QY 96 PAAGAAAG 104
DB 529 AAAAGAAAG 537

RESULT 9
US-09-845-583A-2
/ Sequence 2, Application US/09845583A
/ Patent No. 6635616
/ GENERAL INFORMATION:
/ APPLICANT: Burgess, Robert
/ APPLICANT: Brunken, William Joseph
/ APPLICANT: Champilaud, Marie-France
/ APPLICANT: Hunter, Dale
/ TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
/ FILE REFERENCE: 10287-056001
/ CURRENT APPLICATION NUMBER: US/09/845,583A
/ CURRENT FILING DATE: 2001-04-30
/ PRIOR APPLICATION NUMBER: US 60/200,863
/ PRIOR FILING DATE: 2000-05-01
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 3635
/ TYPE: PRP
/ ORGANISM: Mus musculus
US-09-845-583A-2

Query Match 14.0%; Score 78; DB 2; Length 3635;
Best Local Similarity 30.5%; Pred. No. 33;
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLATQC-STOCP-----TGTAIDGVTND 63
DB 1796 GICVGCQHNTEBDQCCRCRPGFVSSDPSPNPASPCVSCPCPLAVPSPNPAFGCVLRNGRTQ 1855
QY 64 VFDR---SAOCVCKCKPNFYNN 82
DB 1856 CLCRPGYAGASCERCAPGFGN 1877

RESULT 10
US-10-037-417-47
/ Sequence 417, Application US/10037417
/ Patent No. 6903201
/ GENERAL INFORMATION:
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Tcherenev, Velizar T
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Grosse, William M
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Vernet, Corine A.M.
/ APPLICANT: Li, Li
/ APPLICANT: Gorman, Linda
/ APPLICANT: Edinger, Shlomo R
/ APPLICANT: Sciore, Paul
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Malysankar, Uriel M
/ APPLICANT: Rothenberg, Mark
/ APPLICANT: Stone, David J
/ APPLICANT: Boldog, Ferenc L
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Anderson, David W
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Elsen, Andrew J
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-235
/ CURRENT APPLICATION NUMBER: US/10/037,417
/ CURRENT FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/260,018
/ PRIOR FILING DATE: 2001-01-05

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; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-47

Query Match          14.0%; Score 78; DB 2; Length 3635;
Best Local Similarity 30.5%; Pred. No. 33;
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;
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```

QY 21 GICVPCQINRVGSVTN-----AGDLATLATOC-STQCP-----TGTALDDGVT 63
DB 1796 GICVGCQHNTEGDCERCRCRPFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
QY 64 VFDR---SAAQCVKCKPNFYNN 82
DB 1856 CLCRPGYAGASCERCAPGFFGN 1877
```

```

RESULT 11
US-10-037-182-4
; Sequence 4, Application US/10037182
; Patent No. 6933273
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Doi, Masayuki
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-4
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```

Query Match          14.0%; Score 78; DB 2; Length 3635;
Best Local Similarity 30.5%; Pred. No. 33;
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLATOC-STQCP-----TGTALDDGVT 63
DB 1796 GICVGCQHNTEGDCERCRCRPFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
QY 64 VFDR---SAAQCVKCKPNFYNN 82
DB 1856 CLCRPGYAGASCERCAPGFFGN 1877
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```

RESULT 12
US-09-252-991A-28455
; Sequence 28455, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28455
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28455
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```

Query Match          13.9%; Score 77.5; DB 2; Length 862;
Best Local Similarity 26.3%; Pred. No. 6.8;
Matches 20; Conservative 11; Mismatches 18; Indels 27; Gaps 3;

QY 2 AAGGANGNPFANNNARGI--CVPCQINRVGSVTNAGDLATLATATOCSTQCTGTALDD 59
DB 639 AARGSRGARKKSGSDRAQGLGDCIDCQ-----QCVQVCPGTGIDIRD 680
QY 60 GVTDVDFDRSAAQCVK 75
DB 681 GL-----QIACIGC 689
```

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RESULT 13
US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10932
; LENGTH: 3647
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10932
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```

Query Match          13.9%; Score 77.5; DB 2; Length 3647;
Best Local Similarity 27.7%; Pred. No. 38;
Matches 23; Conservative 9; Mismatches 28; Indels 23; Gaps 4;

QY 21 GICVPCQIN-----RVGSVTNAGDLATLATATOCSTQCP-----TGTALDDGVT 62
DB 1812 GVCVDCQHNTEGAHCERCQAGFVSSRDPSTPCVSC--PCPLAVPSNNFADGCVLRNGRT 1869
QY 63 DVFDR---SAAQCVKCKPNFYNN 82
DB 1870 QCLCKPGYAGASCERCAPGFFGN 1892
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RESULT 14
US-08-460-309-19
; Sequence 19, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; NUMBER OF SEQUENCES: 23
; TITLE OF INVENTION: Fragments and Uses Thereof
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-19

Query Match      13.8%; Score 77; DB 1; Length 314;
Best Local Similarity 23.9%; Pred. No. 2.3;
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;

QY 23 CVPQINRVGSVYNAGDLATLATQGST-----QC-----PTGTALD---DSV-TD 63
DB 220 CKAECENKIGSTINDCNVTTGECCKLITNFGDNCRCRKHGYNPTCSYCDNDNGTSE 279

QY 64 VFDRSAQCV-----KCKPNFY 80
DB 280 ICKKSGGQICRGGFGPRDQCLPFGY 307

RESULT 15
US-08-125-077-19
; Sequence 19, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
```

```
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-125-077-19

Query Match      13.8%; Score 77; DB 1; Length 314;
Best Local Similarity 23.9%; Pred. No. 2.3;
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;

QY 23 CVPQINRVGSVYNAGDLATLATQGST-----QC-----PTGTALD---DSV-TD 63
DB 220 CKAECENKIGSTINDCNVTTGECCKLITNFGDNCRCRKHGYNPTCSYCDNDNGTSE 279

QY 64 VFDRSAQCV-----KCKPNFY 80
DB 280 ICKKSGGQICRGGFGPRDQCLPFGY 307

Search completed: December 5, 2005, 06:17:09
Job time : 47 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2005, 06:12:28 ; Search time 165 Seconds

(Without alignments)
265,891 Million cell updates/sec

Title: US-09-196-161d-1

Perfect score: 558
Sequence: 1 GAAAGGANGQFPFANNAAAGC.....PQGEAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main: *
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	442	5	US-10-878-694-5
2	221	39.6	468	5	US-10-878-694-6
3	87.5	15.7	3265	4	US-10-184-644-257
4	87.5	15.7	3265	4	US-10-184-634-257
5	87.5	15.7	3265	4	US-10-063-685-69
6	85.5	15.3	914	3	US-09-975-143-47
7	85.5	15.3	1076	4	US-10-028-072-219
8	85.5	15.3	1076	4	US-10-140-808-219
9	85.5	15.3	1076	4	US-10-121-049-219
10	85.5	15.3	1076	4	US-10-123-904-219
11	85.5	15.3	1076	4	US-10-140-470-219
12	85.5	15.3	1076	4	US-10-175-746-219
13	85.5	15.3	1076	4	US-10-176-918-219
14	85.5	15.3	1076	4	US-10-176-921-219
15	85.5	15.3	1076	4	US-10-137-865-219
16	85.5	15.3	1076	4	US-10-140-474-219
17	85.5	15.3	1076	4	US-10-143-431-219
18	85.5	15.3	1076	4	US-10-143-114-219
19	85.5	15.3	1076	4	US-10-143-419-219
20	85.5	15.3	1076	4	US-10-123-262-219
21	85.5	15.3	1076	4	US-10-143-423-219
22	85.5	15.3	1076	4	US-10-121-050-219
23	85.5	15.3	1076	4	US-10-141-755-219
24	85.5	15.3	1076	4	US-10-143-032-219
25	85.5	15.3	1076	4	US-10-123-108-219
26	85.5	15.3	1076	4	US-10-123-236-219
27	85.5	15.3	1076	4	US-10-123-261-219

28	85.5	15.3	1076	4	US-10-140-921-219	Sequence 219, App
29	85.5	15.3	1076	4	US-10-140-928-219	Sequence 219, App
30	85.5	15.3	1076	4	US-10-121-045-219	Sequence 219, App
31	85.5	15.3	1076	4	US-10-123-292-219	Sequence 219, App
32	85.5	15.3	1076	4	US-10-123-903-219	Sequence 219, App
33	85.5	15.3	1076	4	US-10-124-819-219	Sequence 219, App
34	85.5	15.3	1076	4	US-10-124-822-219	Sequence 219, App
35	85.5	15.3	1076	4	US-10-140-925-219	Sequence 219, App
36	85.5	15.3	1076	4	US-10-160-498-219	Sequence 219, App
37	85.5	15.3	1076	4	US-10-124-824-219	Sequence 219, App
38	85.5	15.3	1076	4	US-10-127-825A-219	Sequence 219, App
39	85.5	15.3	1076	4	US-10-127-829A-219	Sequence 219, App
40	85.5	15.3	1076	4	US-10-127-835A-219	Sequence 219, App
41	85.5	15.3	1076	4	US-10-127-839A-219	Sequence 219, App
42	85.5	15.3	1076	4	US-10-127-901A-219	Sequence 219, App
43	85.5	15.3	1076	4	US-10-128-693A-219	Sequence 219, App
44	85.5	15.3	1076	4	US-10-131-813A-219	Sequence 219, App
45	85.5	15.3	1076	4	US-10-131-818A-219	Sequence 219, App

ALIGNMENTS

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RESULT 1
US-10-878-694-5
; Sequence 5, Application US/10878694
; Publication No. US20050106164A1
; GENERAL INFORMATION:
; APPLICANT: GAERTIG, Jacek
; APPLICANT: DICKERSON Jr., Harry W.
; APPLICANT: CLARK, Theodore G.
; TITLE OF INVENTION: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
; FILE OF INVENTION: PROTOZOA
; FILE REFERENCE: 235, 00100101
; CURRENT APPLICATION NUMBER: US/10/878,694
; PRIOR FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: US/09/498,612
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,634
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/122,372
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,905
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 60/131,121
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: PCT/US00/02966
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Ichthyophthirius multifiliis
US-10-878-694-5
Query Match      100.0%; Score 558; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1,7e-50;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 GAAAGGANGQFPFANNAAAGCIVPCQINNVGSVTNAGDATTATOCSTCPTGTAIDG 60
Db      56 GAAAGGANGQFPFANNAAAGCIVPCQINNVGSVTNAGDATTATOCSTCPTGTAIDG 115
Oy      61 VTDFDRSAACVCKENFYNGSGPQGEAPGVVFAAGAAAGV 105
Db      116 VTDFDRSAACVCKENFYNGSGPQGEAPGVVFAAGAAAGV 160
RESULT 2
US-10-878-694-6
; Sequence 6, Application US/10878694
```

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/ Publication No. US20050106164A1
/ GENERAL INFORMATION:
/ APPLICANT: GAERTIG, Jacek
/ APPLICANT: DICKERSON Jr., Harry W.
/ APPLICANT: CLARK, Theodore G.
/ APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
/ TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
/ FILE REFERENCE: 235, 00100101
/ CURRENT APPLICATION NUMBER: US/10/878,694
/ PRIOR FILING DATE: 2004-06-28
/ PRIOR APPLICATION NUMBER: US/09/498,612
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/118,634
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: 60/122,372
/ PRIOR FILING DATE: 1999-03-02
/ PRIOR APPLICATION NUMBER: 60/124,905
/ PRIOR FILING DATE: 1999-03-17
/ PRIOR APPLICATION NUMBER: 60/131,121
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: PCT/US00/02966
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 468
/ TYPE: PRT
/ ORGANISM: Ichthyophthirius multifiliis
US-10-878-694-6
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Query Match          39.6%; Score 221; DB 5; Length 468;
Best Local Similarity 53.3%; Pred. No. 8,3e-15;
Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;

QY 17 NAARGICVPCQINRVGSVTNAGDLATLATQCSTGCTGTALDDGV-TDVFDRSAQCCKK 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 NGAATCTACPVNRVCGALTAGNAATIVACNVACPTGALDDGVTTDVFSTFCVKCR 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 PNFFYNGGSPQGEAP 91
DB 191 LNFYNGNN--GNTP 203
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RESULT 3
US-10-184-644-257
/ Sequence 257, Application US/10184644
/ Publication No. US2003004930A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C227
/ CURRENT APPLICATION NUMBER: US/10/184,644
/ PRIOR FILING DATE: 2002-06-28
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 257
/ LENGTH: 3265
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-184-644-257
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Query Match          15.7%; Score 87.5; DB 4; Length 3265;
Best Local Similarity 33.0%; Pred. No. 9.7;
Matches 30; Conservative 4; Mismatches 48; Indels 9; Gaps 4;

QY 14 AANNAARGICVPCQINRVGSVTNAGDLATLATQCSTGCTGTALDDGV-TDVFDRSAQC 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3123 AATTAATAATCATC---TATCTGAGTAGTCAA-AATACAAATGAAGAGAGCAAAATTAAC 3177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 VKCKPFFYNGGSPQGEAPGVQVFAAGAAA 103
DB 3178 AACATT---TGGAAAAAAAAAAAAAAAAA 3205
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RESULT 4
US-10-184-634-257
/ Sequence 257, Application US/10184634
/ Publication No. US20030068684A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C217
/ CURRENT APPLICATION NUMBER: US/10/184,634
/ PRIOR FILING DATE: 2002-06-28
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 257
/ LENGTH: 3265
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-184-634-257
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Query Match          15.7%; Score 87.5; DB 4; Length 3265;
Best Local Similarity 33.0%; Pred. No. 9.7;
Matches 30; Conservative 4; Mismatches 48; Indels 9; Gaps 4;
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QY 14 AANNAARGICVPCQINRVGSVTNAGDLATLATQCSTGCTGTALDDGV-TDVFDRSAQC 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3123 AATTAATAATCATC---TATCTGAGTAGTCAA-AATACAAATGAAGAGAGCAAAATTAAC 3177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 VKCKPFFYNGGSPQGEAPGVQVFAAGAAA 103
DB 3178 AACATT---TGGAAAAAAAAAAAAAAAAA 3205
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RESULT 5
US-10-063-685-69
/ Sequence 69, Application US/10063685
/ Publication No. US20030180909A1
/ GENERAL INFORMATION:
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3230R1C1
/ CURRENT APPLICATION NUMBER: US/10/063,685
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; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 69
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-685-69

Query Match      15.7%; Score 87.5; DB 4; Length 3265;
Best Local Similarity 33.0%; Pred. No. 9.7;
Matches 30; Conservative 4; Mismatches 48; Indels 9; Gaps 4;

QY 14 AANNARGCVCPCQINRVSVTNAGDLATLTCSTQCPTGTALDGV-TDVFDRSAAC 72
DB 3123 AATTAAATCAT----TATCTAGTAGTCA-ATATCAAGTAAGAGACCAATTAAC 3177
QY 73 VKCKPNFYNGSPQGEAPGVFAAGAAAA 103
DB 3178 AACATT---TGAATAAAAAAAAAAAAAA 3205

RESULT 6
US-09-975-143-47
; Sequence 47, Application US/09975143
; Patent No. US20020155513A1
; GENERAL INFORMATION:
; APPLICANT: HSU, Daniel, K.
; APPLICANT: LIU, Fu-Tong
; APPLICANT: DOMLING, Christopher, A.
; TITLE OF INVENTION: GALECTIN EXPRESSION IS INDUCED IN
; FILE REFERENCE: DANHSU.001C1
; CURRENT APPLICATION NUMBER: US/09/975,143
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08561
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 914
; TYPE: PRT
; ORGANISM: human
US-09-975-143-47

Query Match      15.3%; Score 85.5; DB 3; Length 914;
Best Local Similarity 28.6%; Pred. No. 3.8;
Matches 36; Conservative 2; Mismatches 53; Indels 35; Gaps 5;

QY 1 GAAOGEANGQNPFAANNA-----RGICVPCQINRVGSVTN-A 37
DB 595 GAAAGTGGGAACCATTCAAATAACAAGTACTGTTGACCTGACCACTTCAAGTTGCA 654
QY 38 G-DLATLTCSTQCPTGTALDGVTDVFRSAAGCVKCKPNFYNGSPQGEAPGVF 96
DB 655 GTGAATATGCTCCTGTTGCACTA-----CAATCATC-----GGTTAAAAAATCTCA 703
QY 97 AAGAAA 102
DB 704 ATGAAA 709

RESULT 7
US-10-028-072-219
; Sequence 219, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deeneyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
```

```
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR APPLICATION NUMBER: 60/059352
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; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
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; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
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3	PRIOR APPLICATION NUMBER: 60/065186
4	PRIOR FILING DATE: 1997-11-12
5	PRIOR APPLICATION NUMBER: 60/065846
6	PRIOR FILING DATE: 1997-11-17
7	PRIOR APPLICATION NUMBER: 60/066364
8	PRIOR FILING DATE: 1997-11-21
9	PRIOR APPLICATION NUMBER: 60/066453
10	PRIOR FILING DATE: 1997-11-24
11	PRIOR APPLICATION NUMBER: 60/066511
12	PRIOR FILING DATE: 1997-11-24
13	PRIOR APPLICATION NUMBER: 60/066770
14	PRIOR FILING DATE: 1997-11-24
15	PRIOR APPLICATION NUMBER: 60/069212
16	PRIOR FILING DATE: 1997-12-11
17	PRIOR APPLICATION NUMBER: 60/069278
18	PRIOR FILING DATE: 1997-12-11
19	PRIOR APPLICATION NUMBER: 60/069334
20	PRIOR FILING DATE: 1997-12-11
21	PRIOR APPLICATION NUMBER: 60/069694
22	PRIOR FILING DATE: 1997-12-16
23	PRIOR APPLICATION NUMBER: 60/072320
24	PRIOR FILING DATE: 1998-01-23
25	PRIOR APPLICATION NUMBER: 60/073612
26	PRIOR FILING DATE: 1998-02-04
27	PRIOR APPLICATION NUMBER: 60/074086
28	PRIOR FILING DATE: 1998-02-09
29	PRIOR APPLICATION NUMBER: 60/074092
30	PRIOR FILING DATE: 1998-02-09
31	PRIOR APPLICATION NUMBER: 60/077791
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33	PRIOR APPLICATION NUMBER: 60/078910
34	PRIOR FILING DATE: 1998-03-20
35	PRIOR APPLICATION NUMBER: 60/079294
36	PRIOR FILING DATE: 1998-03-25
37	PRIOR APPLICATION NUMBER: 60/079663
38	PRIOR FILING DATE: 1998-02-27
39	PRIOR APPLICATION NUMBER: 60/079728
40	PRIOR FILING DATE: 1998-03-27
41	PRIOR APPLICATION NUMBER: 60/080165
42	PRIOR FILING DATE: 1998-03-31
43	PRIOR APPLICATION NUMBER: 60/081203
44	PRIOR FILING DATE: 1998-04-15
45	PRIOR APPLICATION NUMBER: 60/081818
46	PRIOR FILING DATE: 1998-04-15
47	PRIOR APPLICATION NUMBER: 60/082959
48	PRIOR FILING DATE: 1998-04-24
49	PRIOR APPLICATION NUMBER: 60/083322
50	PRIOR FILING DATE: 1998-04-28
51	PRIOR APPLICATION NUMBER: 60/083545
52	PRIOR FILING DATE: 1998-04-29
53	PRIOR APPLICATION NUMBER: 60/084600
54	PRIOR FILING DATE: 1998-05-07
55	PRIOR APPLICATION NUMBER: 60/084627
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57	PRIOR APPLICATION NUMBER: 60/084637
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59	PRIOR APPLICATION NUMBER: 60/085149
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61	PRIOR APPLICATION NUMBER: 60/085333
62	PRIOR FILING DATE: 1998-05-13
63	PRIOR APPLICATION NUMBER: 60/085338
64	PRIOR FILING DATE: 1998-05-13
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66	PRIOR FILING DATE: 1998-05-13
67	PRIOR APPLICATION NUMBER: 60/085579

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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/086414
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/086430
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/ PRIOR APPLICATION NUMBER: 60/087106
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/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088730
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088741
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088810
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088858
/ PRIOR FILING DATE: 19/98-06-11
/ PRIOR APPLICATION NUMBER: 60/089532
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089599
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089907
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089947
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: 60/090349
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090429
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090445
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090538
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090863
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07

Query Match      15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4

QY      1  GAGGEANGNOFPANNAARGICVCQCQINRVGSYNNAGLTLATQCSQCPGPG---TA 56
Db      469  GAAACAAAGCATCTACCAAGCATCA--GTGAACGTGATATCTCTTCCGATTA 526
QY      57  LDDGVTDVDFDRSAQCCKKPFYNYNGSGPGEAEAPGVYFAAGAAAG 104
Db      527  AAAATATTGGAAAGC-----AGTCAGTAAC--CAAGGCCAAG 563

RESULT 8
US-10-140-808-219
/ Sequence 219, Application US/10140808
/ Publication No. US20030017563A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.

```



```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria A.
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-219
```

```

Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY 1 GAAOGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPFG----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATCTTCTTCCGATTTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAAGCCAAAG 563
```

RESULT 9

```

US-10-121-049-219
; Sequence 219, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-219
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```

Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```

QY 1 GAAOGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPFG----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATCTTCTTCCGATTTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAAGCCAAAG 563
```

RESULT 10

```

US-10-123-904-219
; Sequence 219, Application US/10123904
; Publication No. US2003002238A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-219
```

```

Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY 1 GAAOGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPFG----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATCTTCTTCCGATTTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAAGCCAAAG 563
```

RESULT 11

```

US-10-140-470-219
; Sequence 219, Application US/10140470
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
US-10-140-470-219
```

```
/ APPLICANT: Smith,Victoria
/ APPLICANT: Stewart,Timothy A.
/ APPLICANT: Tumas,Daniel
/ APPLICANT: Matanabe,Colin K
/ APPLICANT: Wood,William
/ APPLICANT: Zhang,Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C160
/ CURRENT APPLICATION NUMBER: US/10/140,470
/ CURRENT FILING DATE: 2002-05-06
/ Prior Application removed - See Palm or File Wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-140-470-219
```

```
Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY      1  GAAAGGANGNPPAANNARGICVPCQINRVSVTNAGDLATLATQCSTQCPTG----TA 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      469  GAAACAAAGAAATCTCAAAAGCCATCA--GTGAAGTGAATATCTTCTTCTCGATTAA 526
```

```
QY      57  LDDGVTVDFRSAAGCVKCKPFYNGSGPGEAPGVFAAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAAAG 563
```

```
RESULT 12
US-10-175-746-219
/ Sequence 219, Application US/10175746
/ Publication No. US20030027270A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Matanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C353
/ CURRENT APPLICATION NUMBER: US/10/175,746
/ CURRENT FILING DATE: 2002-06-19
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-175-746-219
```

```
Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY      1  GAAAGGANGNPPAANNARGICVPCQINRVSVTNAGDLATLATQCSTQCPTG----TA 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

```
Db      469  GAAACAAAGAAATCTCAAAAGCCATCA--GTGAAGTGAATATCTTCTTCTCGATTAA 526
QY      57  LDDGVTVDFRSAAGCVKCKPFYNGSGPGEAPGVFAAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAAAG 563
```

```
RESULT 13
US-10-176-918-219
/ Sequence 219, Application US/10176918
/ Publication No. US20030027275A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Matanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C382
/ CURRENT APPLICATION NUMBER: US/10/176,918
/ CURRENT FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-918-219
```

```
Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY      1  GAAAGGANGNPPAANNARGICVPCQINRVSVTNAGDLATLATQCSTQCPTG----TA 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      469  GAAACAAAGAAATCTCAAAAGCCATCA--GTGAAGTGAATATCTTCTTCTCGATTAA 526
```

```
QY      57  LDDGVTVDFRSAAGCVKCKPFYNGSGPGEAPGVFAAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAAAG 563
```

```
RESULT 14
US-10-176-921-219
/ Sequence 219, Application US/10176921
/ Publication No. US20030027276A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
US-10-176-921-219
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2005, 05:59:29 ; Search time 37 Seconds
(without alignments)
273.048 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558
Sequence: 1 GAAQGEANGNQPPAANNAAR.....PGGEAPGVQVPAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 80:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	395	2 A46031	Immunoblotting sur
2	93	16.7	677	2 C42125	trophozoite cystel
3	84.5	15.1	1737	2 T00209	MEGF8 protein - hu
4	78	14.0	596	2 A45664	variant-specific s
5	78	14.0	3635	2 T10053	laminin alpha 5 ch
6	77.5	13.9	573	2 D83130	probable iron-bulf
7	77	13.8	1372	2 T25933	hypothetical prote
8	77	13.8	3712	2 S18253	laminin alpha-1 ch
9	75.5	13.5	713	2 A35502	major surface-labe
10	75	13.4	1193	2 A44018	laminin B2t chain
11	75	13.4	3084	2 MMMSA	laminin alpha-1 ch
12	72.5	13.0	398	1 S24802	polyferredoxin 6x2
13	72.5	13.0	2225	1 T24063	hypothetical prote
14	72	12.9	109	2 S18333	thyroglobulin - bu
15	71	12.7	610	2 JC7530	vascular apoptosis
16	71	12.7	1713	2 A55347	adhesive ligand ep
17	70.5	12.6	289	2 T25682	hypothetical prote
18	70.5	12.6	1607	1 MMMSA	laminin gamma-1 ch
19	70	12.5	485	2 S36772	E-selectin - bovin
20	69.5	12.5	2824	2 T22759	hypothetical prote
21	69	12.4	1557	2 JC8056	halysase - Gloydiu
22	69	12.4	1557	2 T28811	hypothetical prote
23	68.5	12.3	371	2 C97559	hypothetical prote
24	68.5	12.3	371	2 A42779	conserved hypochet
25	68.5	12.3	425	2 C89753	protein F1C7.3 [1
26	68.5	12.3	484	2 S77602	ccog protein - Par
27	68.5	12.3	962	2 JC5571	subtilisin-like pr
28	68.5	12.3	969	1 A39490	subtilisin-like pr
29	68.5	12.3	975	2 JC5570	subtilisin-like pr

30	68.5	12.3	1280	2 A39117	170K lectin precur
31	68.5	12.3	1895	2 T15881	hypothetical prote
32	68.5	12.3	2014	2 T21560	hypothetical prote
33	68	12.2	738	2 S40992	hypothetical prote
34	68	12.2	739	2 B88553	protein K04H4.2b [
35	67.5	12.1	496	2 F87423	ferredoxin, probab
36	67.5	12.1	932	2 I52527	PAGE4A - mouse (fr
37	67	12.0	294	2 T21668	hypothetical prote
38	67	12.0	315	2 I37383	PAS soluble protei
39	67	12.0	334	2 A40036	apoptosis-mediati
40	67	12.0	439	2 A36385	surface antigen se
41	67	12.0	510	2 AD1554	D-alanine-activati
42	67	12.0	563	2 AB3417	electron-transport
43	67	12.0	1639	1 MMFPB2	laminin gamma-1 ch
44	67	12.0	1827	2 T34288	hypothetical prote
45	67	12.0	3075	2 S14458	laminin alpha-1 ch

ALIGNMENTS

RESULT 1
A46031
Immunoblotting surface I-antigen precursor - Ichthyophthirius multifiliis (fragment)
C/Species: Ichthyophthirius multifiliis
C/Date: 29-Sep-1999 #sequence_revision 29-Sep-1999 #ext_change 09-Jul-2004
C/Accession: A46031
R/Clark, T.G.; McGraw, R.A.; Dickerson, H.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 6363-6367, 1992
A/Title: Developmental expression of surface antigen genes in the parasitic ciliate Ich
A/Reference number: A46031, PMID:92335298; PMID:1631132
A/Accession: A46031
A/Molecule type: mRNA; protein
A/Residues: 1-395 <CLAS>
A/Cross-references: UNIPROT:Q27208; UNIPARC:UP100001/B666; GB:M92907; NID:G3628568; PID:
F:2-395/Product: Immunoblotting surface I-antigen #status experimental <MAT>
A/Note: the authors translated the codon UUG for residue 330 as Ile
A/Note: sequence extracted from NCBI backbone (NCBIN:108734, NCBIPI:108735); the sequenc:
C/Genetic code: SGCS
A/Genetic code: SGCS
C/Keywords: glycoprotein; surface antigen
F:2-395/Product: Immunoblotting surface I-antigen #status experimental <MAT>
F:156,191,245,281/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 558; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAQGEANGNQPPAANNAARGICVPCQINRVGSVTNAGDLATLATQCTGCTGTALDDG 60
DB 37 GAAQGEANGNQPPAANNAARGICVPCQINRVGSVTNAGDLATLATQCTGCTGTALDDG 96
QY 61 VTDFPRAAQCVCCKPFFYNGSGPQGEAPGVQVPAAGAAAGV 105
DB 97 VTDFPRAAQCVCCKPFFYNGSGPQGEAPGVQVPAAGAAAGV 141

RESULT 2
C42125
trophozoite cysteine-rich surface antigen 72 - Giardia lamblia (fragment)
N/Alternate names: CRP72
C/Species: Giardia lamblia
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #ext_change 09-Jul-2004
C/Accession: C42125
R/Adam, R.D.; Yang, Y.M.; Nash, T.E.
Mol. Cell. Biol. 12, 1194-1201, 1992
A/Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 ge
A/Reference number: A42125; PMID:92186850; PMID:1545800
A/Accession: C42125
A/Molecule type: DNA
A/Residues: 1-677 <ADA>
A/Cross-references: UNIPROT:Q7M3R4; UNIPARC:UP100001/B5CF; GB:M63934; NID:G159123
A/Experimental source: trophozoites
A/Note: sequence extracted from NCBI backbone (NCBIN:88443, NCBIPI:88444); this ORF is n

C:Keywords: surface antigen

Query Match 16.7%; Score 93; DB 2; Length 677;

Best Local Similarity 28.4%; Pred. No. 0.22; Mismatches 36; Indels 18; Gaps 4;

Matches 25; Conservative 9; Mismatches 36; Indels 18; Gaps 4;

QY 6 EANGNPP---FAANNAARGICVPCQINRVGSVTNAGDLATLQ--CSTQCPGTALDDGV 61
DB 304 EANKTPGCKTKCKNAKPTCSEC---LDGYNSNGGTGVTCEACGANCATCTQAGND- 358

QY 62 TDVFDNSAAQCVCCKPFFYNGSSPOGE 89
DB 359 -----CKTKCKGFFMKNGPFG 377

RESULT 3

MEGF8 protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1999 #sequence_rev1sion 22-Jan-1999 #text_change 21-Jul-2000

C:Accession: T00209

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A:Reference number: Z14126; MUID:98360089; PMID:9693030

A:Accession: T00209

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1737 <NA>

A:Cross-references: UNIPARC:UPI000006FDFP; EMBL:AB011541; NID:G3449307; PIDN:BAA32469.1;

A:Experimental source: brain; clone HG1392

C:Genetics:

A:Gene: MEGF8

A:Map position: 19q12

Query Match 15.1%; Score 84.5; DB 2; Length 1737;

Best Local Similarity 33.8%; Pred. No. 3.6; Mismatches 28; Indels 17; Gaps 3;

Matches 25; Conservative 4; Mismatches 28; Indels 17; Gaps 3;

QY 21 GICVPCQINRVGSVTNAGDLATLQCSNQCP-----TGTALDDGVTFDPSAAQCVK 74
DB 1267 GKCTKCCCN-----GHADTCNBDDGTCCPCNNTEGTCCGSSPSDRDCKYQCK 1318

QY 75 CKENFYNGSSPOG 88
DB 1319 CRSEFP---GSPFG 1329

RESULT 4

variant-specific surface protein VSP1267 - Giardia lamblia

C:Species: Giardia lamblia

C>Date: 22-Apr-1993 #sequence_rev1sion 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A45664

R:Mowatt, M.R.; Aggarwal, A.; Nash, T.E.

Mol. Biochem. Parasitol. 49, 215-227, 1991

A:Title: Carboxy-terminal sequence conservation among variant-specific surface proteins

A:Reference number: A45664; MUID:92131058; PMID:1775165

A:Accession: A45664

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-596 <NMW>

A:Cross-references: UNIPROT:Q07317; UNIPARC:UPI000016BEE6; GB:M63966; NID:g159140; PID:g

A>Note: sequence extracted from NCBI backbone (NCBIN:77609, NCBI:P:77610)

Query Match 14.0%; Score 78; DB 2; Length 596;

Best Local Similarity 23.0%; Pred. No. 5.7; Mismatches 36; Indels 48; Gaps 6;

Matches 28; Conservative 10; Mismatches 36; Indels 48; Gaps 6;

QY 9 GNPFPANNAARG---ICVPCQINRVGSVTNAGD-----LKT 42
DB 237 GKTHFTTDSAGNKKVCVSGTTNNGGIENCGECTSKESADAGTETCTCKSSNNLSP 296

QY 43 LATQCSQCPGTALDDG-----VTDFDPSAAQCVCCKPFFYNG 83

DB 297 LGDACLTCPAGTAVVSGDSGVCCKPCNHTCAGCQTD--DRETS-CTACYPGSLYLSBN 353

QY 84 GS 85

DB 354 GA 355

RESULT 5

Laminin alpha 5 chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Jul-1999 #sequence_rev1sion 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T10053

R:Miner, J.H.; Lewis, R.M.; Sane, J.R.

submitted to the EMBL Data Library, November 1997

A:Reference number: Z16923

A:Accession: T10053

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3635 <MTN>

A:Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5E8; EMBL:U37501; NID:g2599231; PI

C:Keywords: Basement membrane; cell binding; extracellular matrix

F:1888-1939/Domin: laminin-type EGF-like homology <LEG>

F:1942-1970/Domin: EGF homology <EGF>

Query Match 14.0%; Score 78; DB 2; Length 3635;

Best Local Similarity 30.5%; Pred. No. 31; Mismatches 30; Indels 20; Gaps 4;

Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLQCSNQCP-----TGTALDDGVTFD 63
DB 1796 GICVCGQHTBEGDQCCERCPGVSSDPSPASPCVSCCPPLAVPSNNFADGCVLRNGRTQ 1855

QY 64 VFDR---SNAQCVCCKPFFYNG 82
DB 1856 GICRPGYAGASCERCAPGFGN 1877

RESULT 6

probable iron-sulfur protein PA431 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_rev1sion 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: D83130

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lam,

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: D83130

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-573 <STO>

A:Cross-references: UNIPROT:Q9HMQ0; UNIPARC:UPI000000C5C28; GB:AE004829; GB:AE004091; NIT

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA431

C:Superfamily: nitrogen fixation protein fixG; ferredoxin 2 [4Fe-4S] homology

Query Match 13.9%; Score 77.5; DB 2; Length 573;

Best Local Similarity 26.3%; Pred. No. 6.1; Mismatches 18; Indels 27; Gaps 3;

Matches 20; Conservative 11; Mismatches 18; Indels 27; Gaps 3;

QY 2 AAQGEANGNPFAANNAARGI--CVPCQINRVGSVTNAGDLATLQCSQCPGTGALDD 59
DB 350 AARGSRKARRKGSPPRAQGLGDCIDCQ-----QCQVQVPTGIDIND 391

QY 60 GVTDFDPSAAQCVCCK 75

Db 392 GL-----QIATGCC 400

RESULT 7
T25933
hypothetical protein W02C12.1 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25933
R/Murray, J.; Wohlmann, P.
Submitted to the EMBL Data Library, December 1996
A/Description: The sequence of *C. elegans* cosmid W02C12.
A/Reference number: Z20112
A/Accession: T25933
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1372 <MUR>
A/Cross-references: UNIPROT:P91526; UNIPARC:UPI0000075513; EMBL:U80815; PIDN:AA37995.1
A/Experimental source: strain Bristol N2; clone W02C12
C/Genetics:
A/Gene: CESP:W02C12.1
A/Map position: 4
A/Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 13.8%; Score 77; DB 2; Length 1372;
Best Local Similarity 21.2%; Pred. No. 16;
Matches 28; Conservative 14; Mismatches 50; Indels 40; Gaps 5;

QY 3 AAGEANGNPFANNAARGICVPCQINRVGS-----VTNAGDLATLATQCST 49
Db 1036 SEDECRDECPDEBQLSAGVCPQIGTYSRGNKNCVACPPTTETATMTSTREQCNT 1095
QY 50 Q-----CPTGTALDDGVTVDFDRSAQCCKPNFYNGSGSPGSAFG 92
Db 1096 PKCKPGQFLVETKNGCQCFPRGTQN-----EEGSTCTLCAPD--HTTAAP-GATVAE 1145

QY 93 VQVFAAGAAAG 104
Db 1146 SOCFTSTQCATG 1157

RESULT 8
S18253
laminin alpha-1 chain precursor - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S28399; S18253
R/Kusche-Gullberg, M.; Garlsson, K.; Mackrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A/Title: Laminin A chain: expression during *Drosophila* development and genomic sequence.
A/Reference number: S28399; MUID:93049203; PMID:1425586
A/Accession: S28399
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3712 <KUS>
A/Cross-references: UNIPROT:Q00174; UNIPARC:UPI0000048E1C; GB:M96388; NID:G157799; PIDN:R/Garlsson, K.; Mackrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A/Title: Drosophila laminin A chain: species comparison, and domain structure
A/Reference number: S18253; MUID:92078147; PMID:1744083
A/Accession: S18253
A/Molecule type: mRNA
A/Residues: 1762-7712 <GAR>
A/Cross-references: UNIPARC:UPI0000168C67; EMBL:M75882; NID:G157797; PIDN:AAA28661.1; P/C/Genetics:
A/Gene: FLYBase:Lana
A/Cross-references: FLYBase:FBgn0002526
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F/273-330/Domain: laminin-type EGF-like homology <LEG>
F/333-400/Domain: laminin-type EGF-like homology <LEG2>
F/541-584/Domain: laminin-type EGF-like homology <LEG1>

F/1776-2115/Domain: III <DOM3>
F/1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F/1809-1856/Domain: laminin-type EGF-like homology <LE2>
F/1859-1914/Domain: laminin-type EGF-like homology <LE3>
F/1917-1967/Domain: laminin-type EGF-like homology <LE4>
F/1970-2014/Domain: laminin-type EGF-like homology <LE5>
F/2017-2061/Domain: laminin-type EGF-like homology <LE6>
F/2064-2109/Domain: laminin-type EGF-like homology <LE7>
F/2116-2637/Domain: I/II, heptad repeats <DOM2>
F/2638-3712/Domain: G <DOMG>
F/2698-2863/Domain: repeat G1 <RG1>
F/2864-3048/Domain: repeat G2 <RG2>
F/3049-3223/Domain: repeat G3 <RG3>
F/3079-3200/Domain: laminin G repeat homology <LG3>
F/3334-3528/Domain: repeat G4 <RG4>
F/3529-3712/Domain: repeat G5 <RG5>
F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,

Query Match 13.8%; Score 77; DB 2; Length 3712;
Best Local Similarity 23.9%; Pred. No. 40;
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;

QY 23 CVPCQINRVGSVTNAGDLATLATQCST-----QC-----PTGTALD---DGV-TD 63
Db 492 CKACECKIKGISITNDGCVTTGCECKLTNFGDNCERCKHGYFMYPTCSYCDNDQGTSE 551

QY 64 VFDRSAQCV-----KCKPNFY 80
Db 552 ICKKSGQCTICREGFGGPRCDCLPGFY 579

RESULT 9
A35502
major surface-labeled trophozoite antigen precursor - *Giardia lamblia*
C/Species: *Giardia lamblia*
C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C/Accession: A35502
R/Gillin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So,
Proc. Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990
A/Title: Isolation and expression of the gene for a major surface protein of *Giardia la*
A/Reference number: A35502; MUID:90280395; PMID:2352929
A/Accession: A35502
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-713 <GIL>
A/Cross-references: UNIPROT:P21849; UNIPARC:UPI0000137732; GB:M3641; NID:G159131; PID:R/Gillin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So,
C/Keywords: surface antigen; transmembrane protein

Query Match 13.5%; Score 75.5; DB 2; Length 713;
Best Local Similarity 27.5%; Pred. No. 12;
Matches 28; Conservative 10; Mismatches 35; Indels 29; Gaps 6;

QY 3 AAGEANGNPFANNAARGI--CVPCQINRVGSVTNAGDLATLATQC----- 47
Db 135 ACGDTTGVTIAAGNTYKGIADCAEGCAPATGAEAGKAT-CTKGVSKYLKNDVNCVD 193

QY 48 STQCPGT-----ALDDGVTVDFDRSAQCCKPNFYNGG 84
Db 194 KAQCNSSGTNRKFAVVD-----SENGNKCVCSDNL--NGG 227

RESULT 10
A44018
laminin B2c chain precursor, long form - human
N/Alternate names: cell-adhesive scatter factor ladsln; laminin 10SK chain; nicein 100K
C/Species: *Homo sapiens* (man)
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44018; B44018; S41097; A49401
R/Kallunki, P.; Sainio, K.; Bddy, R.; Byers, M.; Kallunki, T.; Sariola, H.; Beck, K.; H
J. Cell Biol. 119, 679-693, 1992
A/Title: A truncated laminin chain homologous to the B2 chain: structure, spatial expre
A/Reference number: A44018; MUID:93016279; PMID:1183240
A/Accession: A44018

A:Molecule type: mRNA
A:Residues: 1-1193 <KAL>
A:Cross-references: UNIPROT:Q13753; UNIPARC:UPI000003490C; GB:215008; NID:934229; PIDN: C
A:Experimental source: fibroblastoma HT1080 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116635)
A:Accession: B44018
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1109, 'GM' <KA2>
A:Cross-references: UNIPARC:UPI00001466C; GB:215009; GB:547253; NID:934231; PIDN:CAA787
A:Experimental source: fibroblastoma HT1080 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116637)
R:Valley, J.; Verrando, P.; Chamliand, M.F.; Gerecke, D.; Wagman, D.W.; Baudoin, C.; Ab
Eur. J. Biochem. 219, 209-218, 1994
A:Title: The 100-kDa chain of nectin/kalinin is a laminin B2 chain variant.
A:Reference number: S41097; MUID:94139694; PMID:8306988
A:Accession: S41097
A:Molecule type: mRNA
A:Residues: 1-11, 'L', 13-472, 'M', 474-520, 'N', 522-856, 'R', 858-1193 <VA1>
A:Cross-references: UNIPARC:UPI000016ADE1; EMBL:X73902; NID:9452754; PIDN:CAA52108.1; PI
A:Experimental source: keratinocytes
R:Hayazaki, K.; Kikawa, Y.; Nakamura, A.; Yasumitsu, H.; Umeda, M.
Proc. Natl. Acad. Sci. U.S.A. 90, 11767-11771, 1993
A:Title: A large cell-adhesive scatter factor secreted by human gastric carcinoma cells.
A:Reference number: A49401; MUID:94089713; PMID:8265624
A:Accession: A49401
A:Molecule type: protein
A:Residues: 435-441, 'X', 443-444, 'X', 446-449 <MT>
A:Cross-references: UNIPARC:UPI000017C28E
C:Genetic:
A:Gene: GDB:LAMC2; EBR2; EBR2A; L; LAMB2T
A:Cross-references: GDB:136225; OMIM:150292
A:Map position: 1q31-1q31
C:Keywords: alternative splicing; basement membrane; extracellular matrix; glycoprotein
F:1-21/Domain: signal sequence #status predicted <Sig>
F:122-1193/Product: laminin B2 chain #status predicted <MAT>
F:84-128/Domain: laminin-type EGF-like homology <LEG>
F:517-570/Domain: laminin-type EGF-like homology <LEG>

Query Match 13.4%; Score 75; DB 2; Length 1193;
Best Local Similarity 26.7%; Pred. No. 21;
Matches 35; Conservative 11; Mismatches 25; Indels 60; Gaps 9;

QY 20 RGICVPCQINRVGS-----VTNAG---DLATLAT 45
DB 78 RDRCLPCNCKSKSLARCDNSGRCSCKPCVTARCDRLCPGPHMLTDAGCTDDQLKLS 137
QY 46 QCSCTCPTGTALDDGVTVDFDRSAQCVCXKCP-----NYYN--GSGPQGEARG 92
DB 138 KCQCD-PAGIA---GPCD-----AGRCV-CKPAVTGRCDCRSGYYNLGDNPEG---C 184
QY 93 VQVFAAGAAAA 103
DB 185 TQCFYCHSAS 195

RESULT 11
MMMSA
laminin alpha-1 chain precursor - mouse
N:Alternate names: laminin chain A1
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C:Accession: A31771; A30449; S00624; A30450; S08895; S02578; S02790; A30451; S14670
R:Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A:Title: Laminin, a multidomain protein. The A chain has a unique globular domain and ho
A:Reference number: A31771; MUID:89034134; PMID:3182802
A:Accession: A31771
A:Molecule type: mRNA
A:Residues: 1-3084 <SAS>
A:Cross-references: UNIPROT:P19137; UNIPARC:UPI00000278CA; EMBL:J04064; NID:9309419; PID
A:Accession: A30449
A:Molecule type: protein

A:Residues: 183-195, 570-571, 'A', 573-586, 596-612, 'X', 614-617, 'EMK', 630-646, 1217-1222, 'YP
2486; 2624-2639; 2818-2843; 3009-3033, 'V', 3035 <SA2>
A:Cross-references: UNIPARC:UPI0000173C92; UNIPARC:UPI0000173C93; UNIPARC:UPI0000173C94;
C99; UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173C99; UNIPARC:UPI0000173C9C; UNIPARC:UPI000
10000173CA2
R:Harti, L.; Oberbauer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A:Title: The N terminus of laminin A chain is homologous to the B chain.
A:Reference number: S00624; MUID:88225080; PMID:3267223
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208, 'T', 210-334 <HAR>
A:Cross-references: UNIPARC:UPI000016CE8F; EMBL:X07737; NID:952857; PIDN:CAA30561.1; PID
A:Accession: A30450
A:Molecule type: protein
A:Residues: 311-335, 'N', 337-339, 630-642, 'D', 644, 692-734, 737-748, 'X', 750-760, 'G', 762-763,
3-1389; 1449-1459 <HAR2>
A:Cross-references: UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CA5,
CA4; UNIPARC:UPI0000173CAB; UNIPARC:UPI0000173CAC
A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-11e
R:Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A:Reference number: S08895; MUID:89078415; PMID:2462498
A:Accession: S08895
A:Molecule type: protein
A:Residues: 153-169 <MAN>
A:Cross-references: UNIPARC:UPI0000173CAD
R:Fujitawa, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A:Reference number: S02678; MUID:88326259; PMID:2458101
A:Accession: S02678
A:Molecule type: protein
A:Residues: 630-642, 'D', 644, 2690-2704 <FU>
A:Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A:Reference number: S01790; MUID:89030693; PMID:3181157
A:Accession: S01790
A:Molecule type: mRNA
A:Residues: 2538-3084 <DEU>
A:Cross-references: UNIPARC:UPI000016CE8E; EMBL:X13459; NID:955499; PIDN:CAA31807.1; PID
A:Accession: A30451
A:Molecule type: protein
A:Residues: 1911-1929, 1997-2006, 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105, 2120
470; 2487-2498; 2502-2525, 2538-2557, 2561-2591, 'X', 2593-2594; 2600-2610; 2616-2645; 2648-2655,
93; 2998-3005, 'A', 3007-3033, 'V', 3035; 3068-3083 <DE2>
A:Cross-references: UNIPARC:UPI0000173CB6; UNIPARC:UPI0000173CB7; UNIPARC:UPI0000173CB8,
CB7; UNIPARC:UPI0000173CB; UNIPARC:UPI0000173CBF; UNIPARC:UPI0000173CC0; UNIPARC:UPI000
10000173CC6; UNIPARC:UPI0000173CC7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CC9; UNIPAR
A:Note: 2256-Val was also found
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A:Reference number: A34961; MUID:89280632; PMID:2733383
A:Accession: S14670
A:Molecule type: protein
A:Residues: 2424-2436, 2440-2451, 2461-2467, 2487-2525, 2550-2557, 2561-2593, 2600-2610, 2616-2
-2942, 'T', 2944-2964; 2969-2976; 2980-2993; 2998-3000, 'I', 3002-3018, 'V', 3020-3034; 3068-3083
A:Cross-references: UNIPARC:UPI0000173CB9; UNIPARC:UPI0000173CAE; UNIPARC:UPI0000173CB,
CC7; UNIPARC:UPI0000173CB; UNIPARC:UPI0000173CA; UNIPARC:UPI0000173CB; UNIPARC:UPI000
10000173CD1; UNIPARC:UPI0000173CD2; UNIPARC:UPI0000173CD3; UNIPARC:UPI0000173CD4; UNIPAR
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promote
A:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F:25-277/Domain: VI <DOM6>
F:277-331/Domain: laminin-type EGF-like homology <LE01>

F/278-519/Domain: V <DOM5>
F/334-401/Domain: laminin-type EGF-like homology <LE02>
F/404-458/Domain: laminin-type EGF-like homology <LE03>
F/461-507/Domain: laminin-type EGF-like homology <LE04>
F/510-519/Domain: laminin-type EGF-like homology <LE05>
F/520-515/Domain: IYD <DO4B>
F/716-1166/Domain: IYIB <DO3B>
F/716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F/749-795/Domain: laminin-type EGF-like homology <LE07>
F/798-853/Domain: laminin-type EGF-like homology <LE08>
F/830-834/Region: cell adhesion #status predicted
F/856-906/Domain: laminin-type EGF-like homology <LE09>
F/909-955/Domain: laminin-type EGF-like homology <LE10>
F/958-1002/Domain: laminin-type EGF-like homology <LE11>
F/1005-1048/Domain: laminin-type EGF-like homology <LE12>
F/1051-1094/Domain: laminin-type EGF-like homology <LE13>
F/1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
F/1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F/1147-1149/Region: cell attachment (R-G-D) motif
F/1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F/1167-1168/Domain: IVA <DO4A>
F/1369-1561/Domain: IIRA <DO3A>
F/1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F/1410-1466/Domain: laminin-type EGF-like homology <LE18>
F/1459-1513/Domain: laminin-type EGF-like homology <LE19>
F/1516-1560/Domain: laminin-type EGF-like homology <LE20>
F/1562-2133/Domain: IYI <DOM2>
F/1562-2133/Region: heptad repeats
F/2134-3084/Domain: G <DOM3>
F/2150-2308/Domain: laminin G repeat homology <LG1>
F/2137-2452/Domain: laminin G repeat homology <LG2>
F/2218-2683/Domain: laminin G repeat homology <LG3>
F/2452-2897/Domain: laminin G repeat homology <LG4>
F/2925-3082/Domain: laminin G repeat homology <LG5>
F/25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/4579-370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1666,1706,1718
E (Asn) (covalent) #status predicted
F/304-312/Diulfide bonds: #status experimental
F/770,857,1997,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status absent
F/845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 13.4%; Score 75; DB 1; Length 3084;
Best Local Similarity 30.0%; Pred. No. 52;

Matches 21; Conservative 10; Mismatches 31; Indels 8; Gaps 2;

QY 23 CVPQIRVGSVTNAGDLATLQCSYCPGTALDGVTFDPSAQCVCXKRP-NFY 81

Db 1094 CVPQCDLRLPTLCLEGLCSGSDSGTCKENVV-----GPGCKQAGTFAL 1146

QY 82 NGGSPQGEAP 91

Db 1147 RGDNPQGCSP 1156

RESULT 12

S24802 polyferritin 6x2(4Fe-4S) vhub [similarity] - Methanococcus voltae

C/Species: Methanococcus voltae

C/Date: 10-Sep-1999 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C/Accession: S24802

R/Halbach, S.; Klein, A.
submitted to the EMBL Data Library, August 1991

A/Description: Methanococcus voltae harbors two gene groups each of homologous (NiFe) - a

A/Reference number: S16721

A/Accession: S24802

A/Molecule type: DNA

A/Residues: 1-398 <HAL>
A/Cross-references: UNIPROT:Q00388; UNIPARC:UP100000629BE; EMBL:X61204; NID:g1747406; PI
Mol. Gen. Genet. 233, 217-224, 1992
A/Title: Methanococcus voltae harbors four gene clusters potentially encoding two [NiFe]
A/Reference number: A59304; MUID:92293118; PMID:1603063

A/Contents: annotation
C/Genetics:
A/Gene: vhub
C/Superfamily: polyferritin 6x2(4Fe-4S); ferritin 2(4Fe-4S) homology
F/4-52/Domain: ferritin 2(4Fe-4S) homology <FER1>
F/56-109/Domain: ferritin 2(4Fe-4S) homology <FER2>
F/125-179/Domain: ferritin 2(4Fe-4S) homology <FER3>
F/192-247/Domain: ferritin 2(4Fe-4S) homology <FER4>
F/261-329/Domain: ferritin 2(4Fe-4S) homology <FER5>
F/341-395/Domain: ferritin 2(4Fe-4S) homology <FER6>

Query Match 13.0%; Score 72.5; DB 1; Length 398;
Best Local Similarity 27.6%; Pred. No. 13;

Matches 16; Conservative 13; Mismatches 22; Indels 7; Gaps 2;

QY 23 CVPQIRVGSVTNAGDLA-----TLATQCSYCPGTALDGVTFDPSAQCVCXK 75
Db 11 CLVCMNSKACPELEIAIPFKTCLCFSCASACPGALVENNKLIYNS--KCIKC 66

RESULT 13

hypothetical protein W01F3.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T26063

R/Cummings, P.
submitted to the EMBL Data Library, March 1997

A/Reference number: Z20145

A/Accession: T26063

A/Status: preliminary; translated from GB/EMBL/DDB

A/Molecule type: DNA

A/Residues: 1-2225 <WIL>

A/Cross-references: UNIPROT:Q45881; UNIPARC:UP100000816EC; EMBL:Z92815; PTDN:CA07294.1

A/Experimental source: clone W01F3

C/Genetics:
A/Gene: CBSP.W01F3.3

A/Map position: 5
A/Intons: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1

Query Match 13.0%; Score 72.5; DB 2; Length 2225;
Best Local Similarity 28.3%; Pred. No. 67;

Matches 28; Conservative 11; Mismatches 41; Indels 19; Gaps 4;

QY 8 NGNQPFAANAGICVPCQ--INRVGSVTNAGDLATLQCSYCPGTALDGVTFDPSAQCVCXKRP-NFY 81

Db 1862 DGN-----ANNF--GSLDDCQLCLVNIQSIKNGKVAATTAPQITPEEEKLAPGCPG 1915

QY 55 TALDDGVTFDPSAQCVCXKRP-NFYNGGSPQGEAPGV 93

Db 1916 RAPLGSSPYLCCNSAESIGCPTSYCCRRGPPVCCPGV 1954

RESULT 14

S18323 thyroglobulin - bullfrog

C/Species: Rana catesbeiana (bullfrog)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S18323

R/Hayashi, H.; Omiya, Y.; Suzuki, S.
FEBS Lett. 292, 168-170, 1991
A/Title: Tyrosine-130 in bullfrog thyroglobulin is a thyroid hormone generating site.
A/Reference number: S18323; MUID:92070481; PMID:1959601
A/Accession: S18323
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <HAY>
A/Cross-references: UNIPROT:Q7LZ58; UNIPARC:UP10000179E77

Query Match 12.9%; Score 72; DB 2; Length 109;
Best Local Similarity 25.9%; Pred. No. 4.3;
Matches 22; Conservative 12; Mismatches 27; Indels 24; Gaps 4;

```

QY      12 PFAANNARGICVPCQINRVSVTNAGDLATLATQCTGCTALDDGVTVDFDRSAQ 71
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      32 PSAVXQASLKLIL-SRADRIGNVAGCG-----ICPVGSESEDG-----E 69
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      72 CVKCKPFYVNGSGPQG--EAPGVQ 94
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      70 CVPCPHGFYQYKTSPPGMYOKPGVE 94
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 15

```

JC7530
Vascular apoptosis-inducing protein 1 - western diamondback rattlesnake
C:Species: Crotalus atrox (western diamondback rattlesnake)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7530; PC7105
R:Maeda, S.; Ohta, T.; Kaji, K.; Fox, J.W.; Hayashi, H.; Araki, S.
Biochem. Biophys. Res. Commun. 278, 197-204, 2000
A>Title: CDNA cloning and characterization of vascular apoptosis-inducing protein 1.
A:Reference number: JC7530; WUID:20525424; PMID:11071872
A:Contents: Crude venom gland
A:Accession: JC7530
A:Molecule type: mRNA
A:Residues: 1-610 <MAS>
A:Cross-references: UNIPROT:Q9DGB9; UNIPARC:UPI00000FC726; DDBJ:AB042840
A:Accession: PC7105
A:Molecule type: protein
A:Residues: 240-251; 274-283; 378-385; 507-519 <MA2>
A:Cross-references: UNIPARC:UPI0000178FAE; UNIPARC:UPI0000178F80;
C:Comment: This protein, as a homodimeric protein, belongs to snake venom metalloproteas
a specific substrate, induces apoptosis in vascular endothelial cells.
C:Genetics:
A:Gene: VAP1
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: apoptosis

```

```

Query Match      12.7%; Score 71; DB 2; Length 610;
Best Local Similarity 26.7%; Pred. No. 28;
Matches 24; Conservative 11; Mismatches 39; Indels 16; Gaps 4;

```

```

QY      19 ARGICV-PCQINRVSVTNAG----DLATLATQCTGCTALDDGVTVDFDRSAAGV 73
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      444 ABGLCCDQCFKAGAGTECRPAKDECDWADVCTGRSAEC-----IDRFQNGQPC- 492
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      74 KCKPNFYVNGSGPQGEAPGVQVPAAGAAA 103
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      493 KNNNGCYVNGKCPIMADQCIALFGPGATVS 522
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: December 5, 2005, 06:17:54
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 5, 2005, 05:59:29 ; Search time 188 Seconds
(without alignments)
245.398 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558

Sequence: 1 GAAAGCANQNPFAANNAR.....PGCAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	409	3	AB25889 IAG48 (G1
2	558	100.0	442	3	AB25889 IAG48 (G1
3	558	100.0	442	3	AB25889 IAG48 (G1
4	558	100.0	442	3	AB25889 IAG48 (G1
5	297	53.2	89	3	AB25889 IAG48 (G1
6	261	46.2	83	3	AB25889 IAG48 (G1
7	258	46.2	83	3	AB25889 IAG48 (G1
8	221	39.6	468	3	AB25889 IAG48 (G1
9	221	39.6	468	3	AB25889 IAG48 (G1
10	221	39.6	468	3	AB25889 IAG48 (G1
11	221	39.6	468	3	AB25889 IAG48 (G1
12	139	24.9	76	3	AB25889 IAG48 (G1
13	119	21.3	69	3	AB25889 IAG48 (G1
14	102	18.3	72	3	AB25889 IAG48 (G1
15	91	16.3	1755	8	ADP31437 Human sec
16	89	15.9	1464	8	ADP31437 Human sec
17	86	15.4	1464	8	ADP31437 Human sec
18	85.5	15.3	1076	6	ABU6845 Human PRO
19	84.5	15.1	1450	8	AD001059 Mouse hom
20	84.5	15.1	1450	8	AD001059 Mouse hom
21	84.5	15.1	1737	5	AD001057 Human hom
22	84.5	15.1	1774	5	ABG6880 Human REM
23	84.5	15.1	2778	7	ADG51660 Human MEG
24	84.5	15.1	2789	7	ADG51660 Human MEG

ALIGNMENTS

25	84.5	15.1	2854	5	ADH48732 NOV7 prot
26	84	15.1	613	2	AAW73009 Cobra ven
27	84	15.1	621	2	AAW73013 Cobra ven
28	83.5	15.0	70	3	AB25887
29	83.5	15.0	7339	6	AA016358
30	83	14.9	13	3	AB25898
31	83	14.9	70	3	AB25884
32	83	14.9	1190	6	ADA74091 Equine la
33	83	14.9	1849	8	ADP30752 Human sec
34	82	14.7	472	8	ADP31222 Human sec
35	82	14.7	750	8	ADP31131 Human sec
36	81.5	14.6	464	9	AEA42406 Immunogen
37	81.5	14.6	525	8	ADP31227 Human sec
38	80.5	14.4	261	6	ABU21604 Protein e
39	80.5	14.4	1587	9	ADP30579 Human sec
40	80	14.3	267	9	AD247919 Araf-ICAR
41	80	14.3	320	8	ADP31607 Human sec
42	80	14.3	320	8	ADP31649 Human sec
43	79.5	14.2	531	8	ADP31696 Human sec
44	79	14.2	337	8	ADP31387 Human sec
45	79	14.2	2440	9	AB279086 Mouse lam

RESULT 1
AB25889
ID AB25889 standard; protein, 409 AA.
XX
AC AB25889;
XX
DT 18-DEC-2000 (first entry)
XX
DE IAG48 (G1) surface protein amino acid sequence.
XX
KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
KW white spot disease; freshwater fish; immune response; infection control.
XX
OS Ichthyophthirius multifiliis.
XX
PN WO200046373-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000MO-US002962.
XX
PR 04-FEB-1999; 99US-0118634P.
PR 02-MAR-1999; 99US-012372P.
PR 17-MAR-1999; 99US-0124805P.
PR 27-APR-1999; 99US-0131121P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
PA (LINT/) LIN T.
XX
XX Clark TG, Dickerson HW, Lin T;
PI WPI; 2000-506071/45.
DR
XX Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
PT infection in fish.
XX
XX Disclosure; Fig 8; 144p; English.
PS
CC This invention relates to novel i-antigen polypeptide sequences. I-
CC antigens or immobilisation antigens are common to a variety of
CC hymenostomacid ciliates and their expression varies in response to
CC environmental stimuli. This invention relates to i-antigens in
CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite

PR 04-FEB-1999; 99US-0118634P.

PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (CORR.) CORNELL RES FOUND INC.
 PA (CLAR/) CLARK T G.
 PA (DICK/) DICKERSON H W.
 PA (LINT/) LINT T.
 XX
 PI Clark TG, Dickerson HW, Lin T;
 DR WPI, 2000-506071/45.
 XX
 PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
 PT infection in fish.
 XX
 PS Claim 1; Fig 1; 144pp; English.
 XX
 CC This invention relates to novel i-antigen polypeptide sequences. I-
 CC antigens or immobilisation antigens are common to a variety of
 CC hymenocetomid ciliates and their expression varies in response to
 CC environmental stimuli. This invention relates to i-antigens in
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
 CC invention includes two polypeptide and polynucleotide sequences for two i-
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
 CC capable of binding to the nucleotide sequences and a method for
 CC identifying i- multifiliis serotypes using the nucleotide sequences. A
 CC composition (containing the i-antigen nucleotide) capable of eliciting an
 CC immune response in fish is useful for prophylaxis, treatment or for
 CC controlling i- multifiliis infection in fish. Polynucleotide or protein
 CC vaccines comprising a portion of the amplified product encoding an
 CC antigenic i-antigen polypeptide obtained is also useful for treating or
 CC preventing i- multifiliis infection in fish. Sequences AAA97036-A97042,
 CC and AAA97060, AAA97065 and AAA97089 represent i-antigen genes and gene
 CC fragments identified in the invention. Sequences AAA97043-A97064
 CC (including AAA97060) and AAA97071-A97088 represent primers used in the
 CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
 CC AAB25893-B25906 represent i-antigen protein and peptide sequences
 XX
 SQ Sequence 442 AA;
 Query Match 100.0%; Score 558; DB 3; Length 442;
 Best Local Similarity 100.0%; Pred. No.5.1e-51;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 60
 DB 56 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 115
 QY 61 VTDVFDPSAAQCVKCKPNFYNGSSPQGEAPGVQVFAAGAAAGV 105
 DB 116 VTDVFDPSAAQCVKCKPNFYNGSSPQGEAPGVQVFAAGAAAGV 160
 RESULT 4
 AD267374
 ID AD267374 standard; protein; 442 AA.
 AC AD267374;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Ichthyophthirius multifiliis 48 kD antigen protein.
 XX
 KW cloning; protozoacide; vaccine; recombinant polypeptides; protozoa;
 KM ciliate; transgenic cell.
 XX
 OS Ichthyophthirius multifiliis.
 XX
 PN US2005106164-A1.

XX
 XX 19-MAY-2005.
 PD
 XX
 PF 28-JUN-2004; 2004US-00878694.
 XX
 PR 04-FEB-1999; 99US-0118634P.
 PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 PR 04-FEB-2000; 2000US-00498612.
 XX
 PA (GAER/) GAERTIG J.
 PA (DICK/) DICKERSON H W.
 PA (CLAR/) CLARK T G.
 PA (CASS/) CASSIDY-HANLEY D.
 XX
 PI Gaertig J, Dickerson HW, Clark TG, Cassidy-Hanley D;
 DR WPI, 2005-354778/36.
 XX
 PT Producing recombinant polypeptides in Tetrahymena by transforming
 PT Tetrahymena cells with a nucleic acid encoding a recombinant polypeptide,
 PT useful as live vaccines for freshwater fish against infection by
 PT Ichthyophthirius multifiliis.
 XX
 PS Disclosure; SEQ ID NO 5; 66pp; English.
 XX
 CC The invention relates to a method of producing (M1) recombinant
 CC polypeptides (1) in Tetrahymena comprising transforming Tetrahymena cells
 CC with a nucleic acid that encodes a recombinant polypeptide comprising a
 CC vertebrate polypeptide, culturing the transformed Tetrahymena cells to
 CC produce the recombinant polypeptide, and isolating the recombinant
 CC polypeptide. The methods and compositions of the present invention are
 CC useful in the field of recombinant protein production, particularly
 CC recombinant protein production in non-pathogenic protozoa, such as the
 CC ciliate Tetrahymena, and for producing live vaccines for freshwater fish
 CC against infection by Ichthyophthirius multifiliis. The transgenic cells
 CC may also be used to isolate and purify antibodies. This sequence
 CC corresponds to the protein sequence of the Ichthyophthirius multifiliis
 CC 48 kD antigen used in the method of the invention.
 XX
 SQ Sequence 442 AA;
 Query Match 100.0%; Score 558; DB 9; Length 442;
 Best Local Similarity 100.0%; Pred. No.5.1e-51;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 60
 DB 56 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 115
 QY 61 VTDVFDPSAAQCVKCKPNFYNGSSPQGEAPGVQVFAAGAAAGV 105
 DB 116 VTDVFDPSAAQCVKCKPNFYNGSSPQGEAPGVQVFAAGAAAGV 160
 RESULT 5
 AAB25862
 ID AAB25862 standard; protein; 89 AA.
 XX
 AC AAB25862;
 XX
 DT 18-DEC-2000 (first entry)
 XX
 DE 48kD i-antigen repeat amino acid sequence SEQ ID 9.
 XX
 KW Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine;
 KM white spot disease; freshwater fish; immune response; infection control.
 XX
 OS Ichthyophthirius multifiliis.
 XX
 PN WO200046373-A1.

```

PD 10-AUG-2000.
XX
XX 04-FEB-2000; 2000MO-US002962.
XX
XX 04-FEB-1999; 99US-0118634P.
XX 02-MAR-1999; 99US-0122372P.
XX 17-MAR-1999; 99US-0124905P.
XX 27-APR-1999; 99US-0131121P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX (CORR ) CORNELL RES FOUND INC.
XX (CLAR/) CLARK T G.
XX (DICK/) DICKERSON H W.
XX (LINT/) LINT T.
XX
XX Clark TG, Dickerson HW, Lin T;
XX WPI; 2000-506071/45.
XX
XX Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
XX infection in fish.
XX
XX Disclosure; Fig 5a; 144pp; English.
XX
XX This invention relates to novel i-antigen polypeptide sequences. I-
XX antigens or immobilisation antigens are common to a variety of
XX hymenosomatid ciliates and their expression varies in response to
XX environmental stimuli. This invention relates to i-antigens in
XX Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
XX of freshwater fish causing ichthyophthiriasis or white spot disease. The
XX invention includes two polypeptide and polynucleotide sequences for two i
XX -antigens, of 48 and 55 kD. Also included in the invention are antibodies
XX capable of binding to the nucleotide sequences and a method for
XX identifying i. multifiliis serotypes using the nucleotide sequences. A
XX composition (containing the i-antigen nucleotide) capable of eliciting an
XX immune response in fish is useful for prophylaxis, treatment or for
XX controlling i. multifiliis infection in fish. Polynucleotide or protein
XX vaccines comprising a portion of the amplified product encoding an
XX antigenic i-antigen polypeptide obtained is also useful for treating or
XX preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
XX and AA97060, AA97065 and AA97089 represent i-antigen genes and gene
XX fragments identified in the invention. Sequences AA97043-A97064
XX (excluding AA97060) and AA97071-A97088 represent primers used in the
XX isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
XX AAB25893-B25906 represent i-antigen protein and peptide sequences
XX
XX SQ
XX
XX Sequence 89 AA;
XX
XX Query Match 53.2%; Score 297; DB 3; Length 89;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-24;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 CPTGTALDDGVTVDVDFRPSAAQCVCXKPNFYNGSGSQGEAPGVQVFAAGAAAGV 105
XX |||||
XX 1 CPTGTALDDGVTVDVDFRPSAAQCVCXKPNFYNGSGSQGEAPGVQVFAAGAAAGV 55
XX
XX Db
XX
XX RESULT 6
XX AAB25861
XX ID AAB25861 standard; protein; 83 AA.
XX
XX AC AAB25861;
XX
XX DT 18-DEC-2000 (first entry)
XX
XX 48kD i-antigen repeat amino acid sequence SEQ ID 8.
XX
XX Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
XX white spot disease; freshwater fish; immune response; infection control.
XX
XX Ichthyophthirius multifiliis.
XX

```

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PN WO200046373-A1.
XX
XX 10-AUG-2000.
XX
XX 04-FEB-2000; 2000MO-US002962.
XX
XX 04-FEB-1999; 99US-0118634P.
XX 02-MAR-1999; 99US-0122372P.
XX 17-MAR-1999; 99US-0124905P.
XX 27-APR-1999; 99US-0131121P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX (CORR ) CORNELL RES FOUND INC.
XX (CLAR/) CLARK T G.
XX (DICK/) DICKERSON H W.
XX (LINT/) LINT T.
XX
XX Clark TG, Dickerson HW, Lin T;
XX WPI; 2000-506071/45.
XX
XX Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
XX infection in fish.
XX
XX Disclosure; Fig 5a; 144pp; English.
XX
XX This invention relates to novel i-antigen polypeptide sequences. I-
XX antigens or immobilisation antigens are common to a variety of
XX hymenosomatid ciliates and their expression varies in response to
XX environmental stimuli. This invention relates to i-antigens in
XX Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
XX of freshwater fish causing ichthyophthiriasis or white spot disease. The
XX invention includes two polypeptide and polynucleotide sequences for two i
XX -antigens, of 48 and 55 kD. Also included in the invention are antibodies
XX capable of binding to the nucleotide sequences and a method for
XX identifying i. multifiliis serotypes using the nucleotide sequences. A
XX composition (containing the i-antigen nucleotide) capable of eliciting an
XX immune response in fish is useful for prophylaxis, treatment or for
XX controlling i. multifiliis infection in fish. Polynucleotide or protein
XX vaccines comprising a portion of the amplified product encoding an
XX antigenic i-antigen polypeptide obtained is also useful for treating or
XX preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
XX and AA97060, AA97065 and AA97089 represent i-antigen genes and gene
XX fragments identified in the invention. Sequences AA97043-A97064
XX (excluding AA97060) and AA97071-A97088 represent primers used in the
XX isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
XX AAB25893-B25906 represent i-antigen protein and peptide sequences
XX
XX SQ
XX
XX Sequence 83 AA;
XX
XX Query Match 46.8%; Score 261; DB 3; Length 83;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-20;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAQGEANGNQPFPAANNAARGICVPCQINRVGSVTNAGDLATLATQCSTQ 50
XX |||||
XX 34 GAAQGEANGNQPFPAANNAARGICVPCQINRVGSVTNAGDLATLATQCSTQ 83
XX
XX Db
XX
XX RESULT 7
XX AAB25863
XX ID AAB25863 standard; protein; 89 AA.
XX
XX AC AAB25863;
XX
XX DT 18-DEC-2000 (first entry)
XX
XX 48kD i-antigen repeat amino acid sequence SEQ ID 10.
XX
XX Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
XX white spot disease; freshwater fish; immune response; infection control.
XX
XX

```

OS Ichthyophthirius multifiliis.
 XX MO200046373-A1.
 XX
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US002962.
 XX
 PR 04-FEB-1999; 99US-0118634P.
 PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (CORR) CORNELL RES FOUND INC.
 PA (CLAR/) CLARK T G.
 PA (DICK/) DICKERSON H W.
 PA (LINT/) LIN T.
 XX
 PI CLARK TG, Dickerson HW, Lin T;
 DR WPI; 2000-506071/45.
 XX
 PT Novel 1-antigen polypeptides and polynucleotides from Ichthyophthirius
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
 PT infection in fish.
 XX
 PS Disclosure; Fig 5a; 14pp; English.
 XX
 CC This invention relates to novel 1-antigen polypeptide sequences. 1-
 CC antigens or immobilization antigens are common to a variety of
 CC hymenostemal ciliates and their expression varies in response to
 CC environmental stimuli. This invention relates to 1-antigens in
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
 CC invention includes two polypeptide and polynucleotide sequences for two 1
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
 CC capable of binding to the nucleotide sequences and a method for
 CC identifying 1. multifiliis serotypes using the nucleotide sequences. A
 CC composition (containing the 1-antigen nucleotide) capable of eliciting an
 CC immune response in fish is useful for prophylaxis, treatment or for
 CC controlling 1. multifiliis infection in fish. Polynucleotide or protein
 CC vaccines comprising a portion of the amplified product encoding an
 CC antigenic 1-antigen polypeptide obtained is also useful for treating or
 CC preventing 1. multifiliis infection in fish. Sequences AAA97036-A97042,
 CC and AAA97060, AAA97065 and AAA97089 represent 1-antigen genes and gene
 CC fragments identified in the invention. Sequences AAA97043-A97064
 CC (excluding AAA97060) and AAA97071-A97088 represent primers used in the
 CC isolation of the 1-antigen gene sequences. Sequences AAB25859-B25889 and
 CC AAB25893-B25906 represent 1-antigen protein and peptide sequences
 XX
 SQ Sequence 89 AA;
 Query Match 46.2%; Score 258; DB 3; Length 89;
 Best Local Similarity 87.3%; Pred. No. 1,1e-19;
 Matches 48; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 51 CPTGTALDDGVTTDFDRSAACVCKKPNFYNGSGPGGAGVGVFAAGAAAGV 105
 DB 1 CPTGTALDDGVTTDFDRSAACVCKKPNFYNGSGPGGAGVGVFAAGAAAGV 55
 XX
 AC AAY97177;
 XX
 DT 06-AUG-2003 (revised)
 DT 04-DEC-2000 (first entry)
 XX
 DE 55 kDa immobilization antigen.
 XX

KM BTU1, beta-tubulin; protein expression system; negative selection;
 KM pacitaxel sensitivity; cell surface; antigen; protozoa; ciliate;
 KM live vaccine; Ichthyophthirius multifiliis; immobilization-antigen;
 KM 1-antigen; freshwater; fish; protozoacide.
 XX
 OS Ichthyophthirius multifiliis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..468 "Gln encoded by CAR or TAA"
 XX
 PN MO200046381-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US002966.
 XX
 PR 04-FEB-1999; 99US-0118634P.
 PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 XX
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (GAER/) GAERTIG J.
 PA (DICK/) DICKERSON H W.
 PA (CLAR/) CLARK T G.
 XX
 PI Gaertig J, Dickerson HW, Clark TG;
 PT
 DR WPI; 2000-514962/46.
 DR N-PSDB; AAA52136.
 XX
 PT Recombinant expression systems for expressing heterologous nucleic acids
 PT and producing recombinant protein, comprises nonpathogenic protozoa such
 PT as Tetrahymena resistant to pacitaxel.
 XX
 PS Disclosure; Fig 3a; 83pp; English.
 XX
 CC Tetrahymena thermophila expresses two major beta-tubulin genes (BTU1 and
 CC BTU2), which encode identical beta-tubulin proteins. Either of these two
 CC genes (but not both at once) can be disrupted without a detectable change
 CC in the cell phenotype. A K350L substitution in the BTU1 beta-tubulin
 CC protein confers increased resistance to microtubule-stabilizing drugs
 CC and increased sensitivity to pacitaxel, a microtubule-stabilizing drug.
 CC Cells carrying the Btu1-K350M allele can be transformed to pacitaxel
 CC resistance by gene replacement of Btu1-K350M with a wild-type BTU1 gene
 CC fragment, eliminating the need to incorporate a means for positive
 CC selection. Where the host organism is not a T. thermophila mutant
 CC containing the Btu1-K350M allele, BTU1::neol construct, which
 CC substitutes the coding region of the neol gene (conferring resistance to
 CC paromycin) for that of BTU1, can be used to generate BTU1 gene knockouts
 CC and for positive selection. Heterologous nucleic acids (especially
 CC encoding antigenic polypeptides) can be inserted into a BTU gene for
 CC successful cell-surface expression that is maintained by way of negative
 CC selection. Preferred expression vectors disrupt the Btu1-K350M gene by
 CC homologous recombination-mediated insertion of a heterologous nucleic
 CC acid, thereby restoring resistance to pacitaxel in the resulting
 CC transgenic host. Transgenic ciliated protozoa are useful as live vaccines
 CC for stimulating an immune response in a vertebrate. The transgenic
 CC protozoan host cells are also useful for producing polyclonal antibodies
 CC (claimed). In particular, Tetrahymena expressing Ichthyophthirius
 CC multifiliis immobilization-antigen (1-antigen) protein on their surface
 CC are effective vehicles for vaccination of freshwater fish against
 CC infection by 1. multifiliis. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 468 AA;
 Query Match 39.6%; Score 221; DB 3; Length 468;
 Best Local Similarity 53.3%; Pred. No. 6.6e-15;
 Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;
 QY 17 NAARGICVPCQINRVGVTNAGDLATLATGCTGCTGTALDDGVTTDFDRSAACVCKK 76

DB 131 NAGASTCTACPVNRVGALTAGNAATIVAGCNVACPTGTALDDGVTDDVRSFTECVKCR 190
 QY 77 PNFYNGSGSPGGEAP 91
 DB 191 LNFYNGNN--GNTP 203

RESULT 9
 AAB25882
 ID AAB25882 standard; protein; 468 AA.
 AC AAB25882;
 XX
 DT 18-DEC-2000 (first entry)
 DE Synthetic 55kd i-antigen protein L6P.
 XX
 KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
 KM white spot disease; freshwater fish; immune response; infection control.
 XX
 OS Ichthyophthirius multifiliis.
 OS Synthetic.
 XX
 PN WO200046373-A1.
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US002962.
 XX
 PR 04-FEB-1999; 99US-0118634P.
 PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (CORR) CORNELL RES FOUND INC.
 PA (CLAR/) CLARK T G.
 PA (DICK/) DICKERSON H W.
 PA (LINT/) LIN T.
 XX
 PI Clark TG, Dickerson HW, Lin T;
 DR MPI; 2000-506071/45.
 PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
 PT infection in fish.
 XX
 PS Example 5; Fig 14; 144p; English.
 XX

CC This invention relates to novel i-antigen polypeptide sequences. I-
 CC antigens or immobilisation antigens are common to a variety of
 CC hymenostomatid ciliates and their expression varies in response to
 CC environmental stimuli. This invention relates to i-antigens in
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
 CC invention includes two polypeptide and polynucleotide sequences for two i
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
 CC capable of binding to the nucleotide sequences and a method for
 CC identifying i. multifiliis serotypes using the nucleotide sequences. A
 CC composition (containing the i-antigen nucleotide) capable of eliciting an
 CC immune response in fish is useful for prophylaxis, treatment or for
 CC controlling i. multifiliis infection in fish. Polynucleotide or protein
 CC vaccines comprising a portion of the amplified product encoding an
 CC antigenic i-antigen polypeptide obtained is also useful for treating or
 CC preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
 CC and AA97060, AA97065 and AA97089 represent i-antigen genes and gene
 CC fragments identified in the invention. Sequences AA97043-A97064
 CC (excluding AA97060) and AA97071-A97088 represent primers used in the
 CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
 CC AAB25893-B25906 represent i-antigen protein and peptide sequences
 XX

SQ Sequence 468 AA;
 Query Match 39.6%; Score 221; DB 3; Length 468;
 Best Local Similarity 53.3%; Pred. No. 6, 6e-15;
 Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;

QY 17 NARGICVPCQINRVGSVTNAGDLATLATQCSGTCPTGALDDGVTDDVRSAAQCCKK 76
 DB 131 NAGASTCTACPVNRVGALTAGNAATIVAGCNVACPTGTALDDGVTDDVRSFTECVKCR 190
 QY 77 PNFYNGSGSPGGEAP 91
 DB 191 LNFYNGNN--GNTP 203

RESULT 10
 AAB25860
 ID AAB25860 standard; protein; 468 AA.
 AC AAB25860;
 XX
 DT 18-DEC-2000 (first entry)
 DE 55kd i-antigen protein of parasite isolate G5.
 XX
 KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
 KM white spot disease; freshwater fish; immune response; infection control.
 XX
 OS Ichthyophthirius multifiliis.
 OS WO200046373-A1.
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US002962.
 XX
 PR 04-FEB-1999; 99US-0118634P.
 PR 02-MAR-1999; 99US-0122372P.
 PR 17-MAR-1999; 99US-0124905P.
 PR 27-APR-1999; 99US-0131121P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (CORR) CORNELL RES FOUND INC.
 PA (CLAR/) CLARK T G.
 PA (DICK/) DICKERSON H W.
 PA (LINT/) LIN T.
 XX
 PI Clark TG, Dickerson HW, Lin T;
 DR MPI; 2000-506071/45.
 PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
 PT infection in fish.
 XX
 PS Claim 3; Fig 3; 144p; English.
 XX

CC This invention relates to novel i-antigen polypeptide sequences. I-
 CC antigens or immobilisation antigens are common to a variety of
 CC hymenostomatid ciliates and their expression varies in response to
 CC environmental stimuli. This invention relates to i-antigens in
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
 CC invention includes two polypeptide and polynucleotide sequences for two i
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
 CC capable of binding to the nucleotide sequences and a method for
 CC identifying i. multifiliis serotypes using the nucleotide sequences. A
 CC composition (containing the i-antigen nucleotide) capable of eliciting an
 CC immune response in fish is useful for prophylaxis, treatment or for
 CC controlling i. multifiliis infection in fish. Polynucleotide or protein
 CC vaccines comprising a portion of the amplified product encoding an
 CC antigenic i-antigen polypeptide obtained is also useful for treating or
 CC preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
 CC

CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
CC capable of binding to the nucleotide sequences and a method for
CC identifying I. multifiliis serotypes using the nucleotide sequences. A
CC composition (containing the I-antigen nucleotide) capable of eliciting an
CC immune response in fish is useful for prophylaxis, treatment or for
CC controlling I. multifiliis infection in fish. Polynucleotide or protein
CC vaccines comprising a portion of the amplified product encoding an
CC antigenic I-antigen polypeptide obtained is also useful for treating or
CC preventing I. multifiliis infection in fish. Sequences AAA97036-A97042,
CC and AAA97060, AAA97065 and AAA97089 represent I-antigen genes and gene
CC fragments identified in the invention. Sequences AAA97043-A97064
CC (excluding AAA97060) and AAA97071-A97088 represent primers used in the
CC isolation of the I-antigen gene sequences. Sequences AAB25859-B25889 and
CC AAB25893-B25906 represent I-antigen protein and peptide sequences
XX
SQ Sequence 72 AA;

Query Match 18.3%; Score 102; DB 3; Length 72;
Best Local Similarity 53.3%; Pred. No. 0.0042; 9; Indels 0; Gaps 0;
Matches 16; Conservative 5; Mismatches

Qy 51 CPTGTALDDGVTDFDRSAACVCKKPNFY 80
||| ||| ||| : ||| ||| |||
1 CPAGTIVTGGTSTYKQAASECVCANFY 30
Db

RESULT 15
ADP31446
ID ADP31446 standard; protein; 1755 AA.
XX
AC ADP31446;
XX
DT 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #2213.
DE
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
PN MO2004035732-A2.
XX
XX
PD 29-APR-2004.
XX
XX
PF 28-AUG-2003; 2003MO-US026780.
XX
XX 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.

PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467203P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471306P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485225P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kochakota S, Haisan L, Linnemann T;
PI Pierre K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX
PS Claim 1; SEQ ID NO 3444; 428bp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOMB and is not in the specification.
XX
XX
SQ Sequence 1755 AA;

Query Match 16.3%; Score 91; DB 8; Length 1755;
Best Local Similarity 34.6%; Pred. No. 2.5; 48; Indels 18; Gaps 5;
Matches 36; Conservative 2; Mismatches

Qy 1 GAAQGEANGNGPFAANNAARGICVPCQINRVGSVTNAGDLATLATCGTCPTGTALDDG 60

Db 1472 GAAAGAAAGAAAAA--CAAGCTACACTACACCTGGTCAT--TACATTCATATTGGAG 1527
Qy 61 VTDFDRSNAQCVCCKPNFYNGSPQGEAPGVQVPAAGAAAG 104
Db 1528 A-----AATCCAGCTG---TAGCCCAAGG----AAGAGAG 1557

Search completed: December 5, 2005, 06:02:47
Job time : 191 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 5, 2005, 06:16:28 ; Search time 15 Seconds
(Without alignments)
33.518 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep: *
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep: *
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep: *
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep: *
5: /cgn2_6/ptodata/2/pubpaa/PCF_NEW_PUB pep: *
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep: *
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep: *
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85.5	15.3	1076	US-10-131-826A-219	Sequence 219, App
2	72.5	13.0	913	US-10-821-234-1040	Sequence 1040, Ap
3	72.5	13.0	3717	US-10-821-234-1076	Sequence 1076, Ap
4	72	12.9	468	US-11-076-187-2	Sequence 2, Appl
5	69.5	12.5	544	US-10-980-388-40	Sequence 40, Appl
6	69	12.4	396	US-10-467-657-280	Sequence 280, App
7	69	12.4	396	US-10-467-657-4380	Sequence 4380, Ap
8	68.5	12.3	415	US-11-182-946-6	Sequence 6, Appl
9	68.5	12.3	750	US-11-132-285-2	Sequence 2, Appl
10	68.5	12.3	1001	US-11-132-285-40	Sequence 40, Appl
11	68.5	12.3	1013	US-10-131-826A-38	Sequence 38, Appl
12	67	12.0	334	US-10-514-057-6	Sequence 6, Appl
13	67	12.0	335	US-11-182-946-7	Sequence 7, Appl
14	67	12.0	669	US-11-076-187-3	Sequence 3, Appl
15	65	11.6	354	US-10-478-345-2	Sequence 2, Appl
16	64.5	11.6	353	US-10-131-826A-296	Sequence 296, App
17	63.5	11.4	820	US-10-467-657-4910	Sequence 4910, Ap
18	63	11.3	1042	US-11-067-811-1	Sequence 1, Appl
19	62.5	11.2	354	US-10-467-657-6058	Sequence 6058, Ap
20	62.5	11.2	993	US-11-137-465-36	Sequence 36, Appl
21	60.5	10.8	321	US-10-478-345-8	Sequence 8, Appl
22	60.5	10.8	4419	US-10-821-234-1155	Sequence 1155, Ap
23	60	10.8	3500	US-11-085-775-2	Sequence 2, Appl
24	59	10.6	483	US-10-467-657-2774	Sequence 2774, Ap
25	58.5	10.5	964	US-11-137-465-58	Sequence 58, Appl

ALIGNMENTS

26	58.5	10.5	965	7	US-11-113-424-2	Sequence 2, Appl
27	58.5	10.5	965	7	US-11-147-047-51	Sequence 51, Appl
28	58	10.4	251	7	US-11-054-515-1219	Sequence 1219, Ap
29	58	10.4	575	6	US-10-980-388-46	Sequence 46, Appl
30	57.5	10.3	248	7	US-11-080-628-23	Sequence 23, Appl
31	57.5	10.3	7968	7	US-11-186-731-5	Sequence 5, Appl
32	57	10.2	961	7	US-11-113-424-35	Sequence 35, Appl
33	56.5	10.1	228	6	US-10-980-388-17	Sequence 17, Appl
34	56.5	10.1	357	6	US-10-478-345-6	Sequence 6, Appl
35	56.5	10.1	359	7	US-11-105-172-2	Sequence 340, Appl
36	56.5	10.1	386	6	US-10-131-826A-340	Sequence 320, App
37	56	10.0	250	6	US-10-131-826A-320	Sequence 11, Appl
38	56	10.0	255	7	US-11-182-946-11	Sequence 3516, Ap
39	56	10.0	395	6	US-10-467-657-3516	Sequence 46, Appl
40	56	10.0	493	7	US-11-137-465-46	Sequence 35, Appl
41	56	10.0	897	7	US-11-137-465-35	Sequence 84, Appl
42	56	10.0	2004	6	US-10-467-657-84	Sequence 6322, Ap
43	56	10.0	2004	6	US-10-467-657-6322	Sequence 1116, Ap
44	56	10.0	5405	7	US-11-108-172-1116	Sequence 2075, Ap
45	55.5	9.9	246	7	US-11-054-515-2075	

RESULT 1
US-10-131-826A-219
; Sequence 219, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.


```
RESULT 5
US-10-980-388-40
; Sequence 40, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebach, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-40

Query Match          12.5%; Score 69.5; DB 6; Length 544;
Best Local Similarity 25.7%; Pred. No. 1.2; Indels 23; Gaps 3;
Matches 28; Conservative 3; Mismatches 55;

QY 1 GAAQGEANGNQPPAANNAAGICVPCQINRVGSVTNAGDLATLATQCTGCTGTAALDDG 60
DB 403 GATTTCTGTATTCTTCATACCACTGTTATG---ATAATCTTACAGTAAGAT 458
      |||
QY 61 VTDFPDR-----SAAQCCKKKNFYNGSSPQGEAPGVQVFAAGAAAG 104
DB 459 TTTTCTTAGCTAAACAC-----AACCTATAAAATTTG 493
      |||
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RESULT 6
US-10-467-657-280
; Sequence 280, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

RESULT 7
US-10-467-657-4380
; Sequence 4380, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4380
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4380

Query Match          12.4%; Score 69; DB 6; Length 396;
Best Local Similarity 22.5%; Pred. No. 0.94; Indels 20; Gaps 2;
Matches 18; Conservative 12; Mismatches 30;

QY 25 PCQINRVGSVTNAGDLATLATQCTGCTGTAALDDGVTVFDRSAACVCKKKNFYNG 84
DB 311 PCQI-----CTHCCPVQALAPEG--DIHNECTICLHCQVMYHDDR 350
      |||
QY 85 SPQGEAPGVQVFAAGAAAG 104
DB 351 CPQVVAENKKKQKQAAAKSG 370
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RESULT 8
US-11-182-946-6
; Sequence 6, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
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Query Match	12.0%;	Score 67;	DB 6;	Length 334;
Best Local Similarity	26.7%;	Pred. No. 1.3;		
Matches	20;	Conservative 12;	Mismatches 29;	Indels 14;
				Gaps 4;

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RESULT 14
US-11-076-187-3
/ Sequence 3, Application US/11076187
/ Publication No. US20050244857A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni, Jian
/ APPLICANT: Rosen, Craig A
/ APPLICANT: Pan, James G
/ APPLICANT: Gentz, Reiner L
/ APPLICANT: Dixit, Vishva M
/ TITLE OF INVENTION: Death Domain Containing Receptor-4
/ FILE REFERENCE: P/355P3
/ CURRENT APPLICATION NUMBER: US/11/076,187
/ CURRENT FILING DATE: 2005-03-10
/ PRIOR APPLICATION NUMBER: 60/035,722
/ PRIOR FILING DATE: 1997-01-28
/ PRIOR APPLICATION NUMBER: 60/037,829
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 09/013,895
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: 60/132,922
/ PRIOR FILING DATE: 1999-05-06
/ PRIOR APPLICATION NUMBER: 09/565,918
/ PRIOR FILING DATE: 2000-05-05
/ PRIOR APPLICATION NUMBER: 60/406,922
/ PRIOR FILING DATE: 2002-08-30
/

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/ PRIOR APPLICATION NUMBER: 60/413,861
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: 10/648,786
/ PRIOR FILING DATE: 2003-08-27
/ PRIOR APPLICATION NUMBER: 60/551,768
/ PRIOR FILING DATE: 2004-03-11
/ PRIOR APPLICATION NUMBER: 60/608,469
/ PRIOR FILING DATE: 2004-09-10
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 3
/ LENGTH: 669
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-076-187-3
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Query Match      12.0%; Score 67; DB 7; Length 669;
Best Local Similarity 26.7%; Pred. No. 2.7;
Matches 20; Conservative 12; Mismatches 29; Indels 14; Gaps 4;
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```
QY      8  NGNPFANNAAGICVPCOINRVSVTNAGDLATLATGCGPTGTALDDGVTDFDR 67
DB      76  NGDEP-----DCVPCOEGK--EYTDKAHFSSKCRRCRL--CDGSHGLEVEIN--CTR 121
QY      68  SAAQCVKCKENFYNN 82
DB      122  TQNTKCRCKENPFQCN 136
```

```
RESULT 15
US-10-478-345-2
/ Sequence 2, Application US/10478345
/ Publication No. US20050255115A1
/ GENERAL INFORMATION:
/ APPLICANT: Institute of Genetics and Devel. Biol, CAS
/ APPLICANT: Dongguan HaoFa Biotechnology Developmental Co., Ltd.
/ APPLICANT: Beijing ABT Genetic Engineering Technology Co., Ltd.
/ TITLE OF INVENTION: Anti Human Ovarian Cancer- Anti CD3 Bispecific Antibody
/ FILE REFERENCE: L53.2-11393-US01
/ CURRENT APPLICATION NUMBER: US/10/478,345
/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: CN 0118247.4
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: PCT/CN02/00347
/ PRIOR FILING DATE: 2002-05-23
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: AA Seq of VH against human ovarian cancer
US-10-478-345-2
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Query Match      11.6%; Score 65; DB 6; Length 354;
Best Local Similarity 25.2%; Pred. No. 2.2;
Matches 29; Conservative 3; Mismatches 43; Indels 40; Gaps 5;
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```
QY      1  GAAQGEANGNQPFAANNAGICVPCOINRVSVTNAGDLATLATGCGPTGTALDDG 60
DB      44  GAGAGACAGT---CAGGATCTCTGCAAGGCTTCTGGG---TATACCTTC----- 87
QY      61  VTVDVFRSAAQCVKCKENFYNGSPG-----EAPGVQVFAAGAAAG 104
DB      88  -----ACAACTGC-----TGGAATGCAGTGGGTGCACAAAGATGCCAGGAAAG 129
```

Search completed: December 5, 2005, 06:21:26
Job time : 16 secs